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(54) Title: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS USING ARRAYS OF CANDIDATE GENES

(57) Abstract: The invention relates to a polynucleotide library useful in the molecular characterization of a carcinoma, the library including a pool of polynucleotide sequences of subsequences thereof wherein the sequences of subsequences are overpressed in tumor cells, further wherein the sequences of subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID NOS: 1-468 or the complement thereof. The invention relates also to polynucleotide arrays useful to differentiate tumor cells from normal cells comprising combinations of selected immobilized polynucleotide sequences sets.

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GENE EXPRESSION PROFILING OF PRIMARY BREAST
CARCINOMAS USING ARRAYS OF CANDIDATE GENES

5 This invention relates to polynucleotide analysis
and, in particular, to polynucleotide expression profiling of
carcinomas using arrays of candidate polynucleotides.

10 Pathologists and clinicians in charge of the
management of breast cancer patients are facing two major
problems, namely the extensive heterogeneity of the disease
and the lack of factors - among conventional histological and
clinical features - predicting with reliability the evolution
of the disease and its sensitivity to cancer therapies.
Breast tumors of the same apparent prognostic type vary
widely in their responsiveness to therapy and consequent
15 survival of the patient. New prognostic and predictive
factors are needed to allow an individualization of therapy
for each patient.

20 Great hope is currently being placed on molecular
studies, which address the problem in a global fashion.
Methods such as cytogenetics, comparative genomic
hybridization, and whole-genome allelotyping have addressed
the issue at the genome level. Currently, the modifications
that take place in human tumors at the level of transcription
can also be studied in a large, unprecedented scale, using
25 new methods such as cDNA arrays that allow quantitative
measurement of the mRNA expression levels of many genes
simultaneously. Thus, it would be advantageous to provide a
means to assess the capacity of cDNA array testing in
clinical practice to better classify an heterogeneous cancer
30 into tumor subtypes with more homogeneous clinical outcomes,
and to identify new potential prognostic factors and
therapeutics targets.

The invention relates to a polynucleotide library useful in the molecular characterization of a carcinoma, the library including a pool of polynucleotide sequences or subsequences thereof wherein the sequences or subsequences are either underexpressed or overpressed in tumor cells, further wherein the sequences or subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 468 or the complement thereof.

Fig. 1 shows an example of differential gene expression between normal breast tissue (NB) and breast tumor samples.

Fig. 2 is a representation of expression levels of 176 genes in normal breast tissue (NB) and 34 samples of breast carcinoma.

Fig. 3 is prognostic classification of breast cancer by gene expression profiling.

Fig. 4 shows the correlation of GATA3 expression with ER phenotype.

In the context of this disclosure, a number of terms shall be utilized.

The term "polynucleotide" refers to a polymer of RNA or DNA that is single-stranded, optionally containing synthetic, non-natural or altered nucleotide bases. A polynucleotide in the form of a polymer of DNA may be comprised of one or more segments of cDNA, genomic DNA or synthetic DNA.

The term "subsequence" refers to a sequence of nucleic acids that comprises a part of a longer sequence of nucleic acids.

The term "immobilized on a support" means bound directly or indirectly thereto including attachment by

covalent binding, hydrogen bonding, ionic interaction, hydrophobic interaction or otherwise.

Breast cancer is characterized by an important histoclinical heterogeneity that currently hampers the selection of the most appropriate treatment for each case. This problem could be solved by the identification of new parameters that better predict the natural history of the disease and its sensitivity to treatment. An important object of the present invention relates to a large-scale molecular characterization of breast cancer that could help in prediction, prognosis and cancer treatment.

An important aspect of the invention relates to the use of cDNA arrays, which allows to quantitative study mRNA expression levels of 188 candidate genes in 34 consecutive primary breast carcinomas along three directions: comparison of tumor samples, correlations of molecular data with conventional histoclinical prognostic features and gene correlations. The experimentation evidenced extensive heterogeneity of breast tumors at the transcriptional level. Hierarchical clustering algorithm identified two molecularly distinct subgroups of tumors characterized by a different clinical outcome after chemotherapy. This outcome could not have been predicted by the commonly used histoclinical parameters. No correlation was found with the age of patients, tumor size, histological type and grade. However, expression of genes was differential in tumors with lymph node metastasis and according to the estrogen receptor status; ERBB2 expression was strongly correlated with the lymph node status ($p \leq 0.0001$) and that of GATA3 with the presence of estrogen receptors ($p \leq 0.001$). Thus, experimental results identified new ways to group tumors according to outcome and new potential targets of carcinogenesis. They show that the systematic use of cDNA

array testing holds great promise to improve the classification of breast cancer in terms of prognosis and chemosensitivity and to provide new potential therapeutic targets.

5 DNA arrays consist of large numbers of DNA molecules spotted in a systematic order on a solid support or substrate such as a nylon membrane, glass slide, glass beads or a silicon chip. Depending on the size of each DNA spot on the array, DNA arrays can be categorized as microarrays (each
10 DNA spot has a diameter less than 250 microns) and macroarrays (spot diameter is greater than 300 microns). When the solid substrate used is small in size, arrays are also referred to as DNA chips. Depending on the spotting technique used, the number of spots on a glass microarray can
15 range from hundreds to thousands.

DNA microarrays have serve a variety of purposes, including, gene expression profiling, de novo gene sequencing, gene mutation analysis, gene mapping and genotyping. cDNA microarrays are printed with distinct cDNA
20 clones isolated from cDNA libraries. Therefore, each spot represents an expressed gene, since it is derived from a distinct mRNA.

Typically, a method of monitoring gene expression involves providing (1) providing a pool of sample
25 polynucleotides comprising RNA transcript(s) of one or more target gene(s) or nucleic acids derived from the RNA transcript(s); (2) reacting, such as hybridizing the sample polynucleotide to an array of probes (for example, polynucleotides obtained from a polynucleotide library)
30 (including control probes) and (3) detecting the reacted/hybridized polynucleotides. Detection can also involve calculating/quantifying a relative expression (transcription) level.

The present invention concerns a polynucleotide library useful in the molecular characterization of a carcinoma, said library comprising a pool of polynucleotide sequences or subsequences thereof wherein said sequences or subsequences are either underexpressed or overpressed in tumor cells, further wherein said sequences or subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID Nos: 1 - 468 in annex or the complement thereof.

Obviously, sequences having a great degree of homology with the above sequences could also been used to realize the molecular characterization of the invention, namely when those sequences present one or a few punctual mutations when compared with anyone of sequences SEQ ID Nos: 1 - 468.

The invention concerns a polynucleotide library useful in the molecular characterization of a carcinoma, said library comprising a pool of polynucleotide sequences or subsequences thereof wherein said sequences or subsequences are overpressed in tumor cells, further wherein said sequences or subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 249 (Here, these SEQ ID N° refer to old SEQ ID N° 1-249 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex) or the complement thereof

Preferably the pool of polynucleotide sequences or subsequences correspond substantially to the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 247 (Here, these SEQ ID N° refer to old SEQ ID N° 1-247 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application

in annex); further wherein said sequences are useful in differentiating a normal cell from a cancer cell.

5 The invention relates also to a polynucleotide library wherein the pool of polynucleotide sequences or subsequences correspond substantially to the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 242 (Here, these SEQ ID N° refer to old SEQ ID N° 1-242 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex);
10 wherein said sequences are useful in detecting a hormone sensitive tumor cell, or wherein said sequences are useful in differentiating a tumor with lymph nodes from a tumor without lymph nodes.

15 The invention relates also to a polynucleotide library wherein the pool of polynucleotide sequences or subsequences correspond substantially to the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 224; (Here, these SEQ ID N° refer to old SEQ ID N° 1-224 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex) wherein said sequences are useful in differentiating tetracycline-sensitive tumors from tetracycline-insensitive tumors.

25 The invention relates also to any polynucleotide library as previously described wherein said polynucleotides are immobilized on a solid support in order to form a polynucleotide array.

30 Preferably the support is selected from the group consisting of a nylon membrane, glass slide, glass beads, or a silicon chip.

The invention concerns also a method for detecting differentially expressed polynucleotide sequences which are correlated with a cancer, said method comprising:

- a) obtaining a polynucleotide sample from a patient; and
- 5 b) reacting the sample polynucleotide obtained in step (a) with a probe immobilized on a solid support wherein said probe comprises any of the polynucleotide sequences of the libraries previously described or an expression product encoded by any of the polynucleotide sequences of said
- 10 libraries and
- c) detecting the reaction product of step (b).

The invention relates also to a such method for detecting differentially expressed polynucleotide sequences

15 of the invention wherein the amount of reaction product of step (c) is compared to a control sample.

Preferably the polynucleotide sample isolated for, the sample is RNA or mRNA.

Preferably the polynucleotide sample is cDNA obtained by

20 reverse transcription of the mRNA.

In a preferred embodiment the method for detecting differentially expressed polynucleotide sequences, the step

 (b) comprises a hybridization of the sample RNA with the labeled probe.

25 The method for detecting differentially expressed polynucleotide sequences is used for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating conditions associated with cancer, and namely breast cancer.

30 The method for detecting differentially expressed polynucleotide sequences is particular useful wherein the product encoded by any of the polynucleotide sequences or

subsequences is involved in a receptor-ligand reaction on which detection is based.

5 The invention relates also to a method for screening an anti-tumor agent comprising the method for detecting differentially expressed polynucleotide sequences previously described wherein the sample has been treated with the anti-tumor agent to be screened.

10 The label used to label polynucleotide samples is selected from the group consisting of radioactive, colorimetric, enzymatic, molecular amplification, bioluminescent or fluorescent label.

15 The invention also relates to a library of polynucleotides comprising a population of polynucleotide sequences overexpressed or underexpresses in cells derived from a tumor selected from SEQ ID NO :1 to SEQ ID NO :249 and their respective complements. (Here, these SEQ ID N° refer to old SEQ ID N° 1-249 in priority document, the correlation
20 table 10 allows to identify these sequences in the sequence listing of the present application in annex).

In a particular embodiment the invention relates to polynucleotide sequences: SEQ ID No : 1 ; SEQ ID No : 5 ;
25 SEQ ID No : 8 ; SEQ ID No : 9 ; SEQ ID No : 28 ; SEQ ID No : 29 ;
SEQ ID No : 30 ; SEQ ID No : 31 ; SEQ ID No : 32 ; SEQ ID No : 45 ;
SEQ ID No : 46 ; SEQ ID No : 52 ; SEQ ID No : 54 ; SEQ ID No : 63 ;
SEQ ID No : 64 ; SEQ ID No : 81 ; SEQ ID No : 82 ; SEQ ID No : 87 ;
SEQ ID No : 88 ; SEQ ID No : 101 ; SEQ ID No : 102 ; SEQ ID
30 No : 103 ; SEQ ID No : 104 ; SEQ ID No : 105 ; SEQ ID No : 107 ;
SEQ ID No : 113 ; SEQ ID No : 114 ; SEQ ID No : 115 ; SEQ ID No : 116 ;
SEQ ID No : 127 ; SEQ ID No : 128 ; SEQ ID No : 131 ; SEQ ID No : 139 ;
SEQ ID No : 140 ; SEQ ID No : 142 ; SEQ ID No : 150 ;
SEQ ID No : 151 ; SEQ ID No : 154 ; SEQ ID No : 156 ; SEQ ID

No : 160 ; SEQ ID No : 161 ; SEQ ID No : 162 ; SEQ ID No : 177 ;
SEQ ID No : 178 ; SEQ ID No : 194 ; SEQ ID No : 195 ; SEQ ID No :
227 ; SEQ ID No : 228 ; SEQ ID No : 229 ; SEQ ID No : 231 ; SEQ ID
No : 233 ; SEQ ID No : 243 ; SEQ ID No : 244 ; SEQ ID No : 245 ;
5 SEQ ID No : 246 ; SEQ ID No : 247, (Here, these SEQ ID N° refer
to old SEQ ID N° presented on table 5 in priority document,
the correlation table 10 allows to identify these sequences
in the sequence listing of the present application in annex),
which distinguish a healthy person from a person with cancer.

10 Preferably the invention relates to
polynucleotide sequences: SEQ ID No : 1 ; SEQ ID No : 5 ; SEQ ID
No : 102 ; SEQ ID No : 103 ; SEQ ID No : 107 ; SEQ ID No : 229 ;
SEQ ID No : 45 ; SEQ ID No : 46 ; SEQ ID No : 243 ; SEQ ID No :
244 ; SEQ ID No : 245 ; SEQ ID No : 246 ; SEQ ID No : 247 (Here,
15 these SEQ ID N° refer to old SEQ ID N° presented on table 6
in priority document, the correlation table 10 allows to
identify these sequences in the sequence listing of the
present application in annex), which distinguish a healthy
person from a person with cancer.

20 In another particular embodiment the invention relates
to polynucleotide sequences: SEQ ID No : 2 ; SEQ ID No : 3 ;
SEQ ID No : 4 ; SEQ ID No : 5 ; SEQ ID No : 6 ; SEQ ID No : 7 ;
SEQ ID No : 8 ; SEQ ID No : 9 ; SEQ ID No : 10 ; SEQ ID No : 11 ;
25 SEQ ID No : 12 ; SEQ ID No : 13 ; SEQ ID No : 14 ; SEQ ID No : 15
; SEQ ID No : 16 ; SEQ ID No : 17 ; SEQ ID No : 18 ; SEQ ID No :
19 ; SEQ ID No : 20 ; SEQ ID No : 21 ; SEQ ID No : 22 ; SEQ ID No
: 23 ; ; SEQ ID No : 24 ; SEQ ID No : 25 ; SEQ ID No : 26 ; SEQ ID
No : 27 ; SEQ ID No : 221 ; SEQ ID No : 222 ; SEQ ID No : 223 ;
30 SEQ ID No : 241 ; SEQ ID No : 242 (Here, these SEQ ID N° refer
to old SEQ ID N° presented on table 7 in priority document,
the correlation table 10 allows to identify these sequences
in the sequence listing of the present application in annex)
which detect hormone sensitive tumors.

Preferably the invention relates to polynucleotide sequences SEQ ID No : 1; SEQ ID No : 2 SEQ ID No : 3; SEQ ID No : 4; SEQ ID No : 5; SEQ ID No : 221; SEQ ID No : 222 ; SEQ ID No : 15; SEQ ID No : 16; SEQ ID No : 17; SEQ ID No : 18 ; SEQ ID No : 19; SEQ ID No : 20 ; SEQ ID No : 21; SEQ ID No : 22 ; SEQ ID No : 241; SEQ ID No : 242 (Here, these SEQ ID N° refer to old SEQ ID N° presented on table 8 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex), which detect hormone sensitive tumors.

In another particular embodiment the invention relates to polynucleotide sequences: SEQ ID No : 1 ; SEQ ID No : 3 ; SEQ ID No : 4 ; SEQ ID No : 19 ; SEQ ID No : 20 ; SEQ ID No : 21; SEQ ID No : 22 ; SEQ ID No : 23 ; SEQ ID No : 26 ; SEQ ID No : 27 ; SEQ ID No : 28 ; SEQ ID No : 29 ; SEQ ID No : 30 ; SEQ ID No : 31 ; SEQ ID No : 32 ; SEQ ID No : 33 ; SEQ ID No : 34 ; SEQ ID No : 35 ; SEQ ID No : 36; SEQ ID No : 37; SEQ ID No : 38; SEQ ID No : 39; SEQ ID No : 40 ; SEQ ID No : 41 ; SEQ ID No : 42 ; SEQ ID No : 43 ; SEQ ID No : 44 ; SEQ ID No : 221 ; SEQ ID No : 222 ; SEQ ID No : 233 ; SEQ ID No : 241 ; SEQ ID No : 242 (Here, these SEQ ID N° refer to old SEQ ID N° presented on table 8 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex), which distinguish tumors with lymph node from tumors with no lymph node.

Preferably the invention relates to polynucleotide sequences : SEQ ID No : 1 ; SEQ ID No : 21 ; SEQ ID No : 22 ; SEQ ID No : 28; ; SEQ ID No : 29 ; SEQ ID No : 29 ; SEQ ID No : 31 ; SEQ ID No : 32 ; SEQ ID No : 19 ; SEQ ID No : 20 ; SEQ ID No : 26 ; SEQ ID No : 27 ; SEQ ID No : 37 ; SEQ ID No : 38 ; SEQ ID No : 39 ; SEQ ID No : 241 ; SEQ ID No : 241, (Here, these SEQ ID N° refer to old SEQ ID N° presented on table 8 in priority document, the correlation table 10 allows to

identify these sequences in the sequence listing of the present application in annex), which distinguish tumors with lymph node from tumors with no lymph node.

5 In another particular embodiment the invention relates to polynucleotide sequences: SEQ ID No : 1 ; SEQ ID No : 2 ;
SEQ ID No : 6 ; SEQ ID No : 7 ; SEQ ID No : 8 ; SEQ ID No : 9 ;
SEQ ID No : 10 ; SEQ ID No : 11 ; SEQ ID No : 13 ; SEQ ID No : 14
10 ; SEQ ID No : 19 ; SEQ ID No : 20 ; SEQ ID No : 21 ; SEQ ID No :
22 ; SEQ ID No : 23 ; SEQ ID No : 35 ; SEQ ID No : 36 ; ; SEQ ID
No : 37 ; SEQ ID No : 56 ; SEQ ID No : 57 ; SEQ ID No : 74 ; SEQ
ID No : 75 ; SEQ ID No : 102 ; SEQ ID No : 104 ; SEQ ID No : 107
; SEQ ID No : 108 ; SEQ ID No : 109 ; SEQ ID No : 118 ; SEQ ID No
: 119 ; ; SEQ ID No : 136 ; SEQ ID No : 213 ; SEQ ID No : 214 ;
15 SEQ ID No : 215 ; SEQ ID No : 223 ; SEQ ID No : 224 (Here, these
SEQ ID N° refer to old SEQ ID N° presented on table 11 in
priority document, the correlation table 10 allows to
identify these sequences in the sequence listing of the
present application in annex) which distinguish tumors
20 sensitive to anthracycline from tumors unsensitive to
anthracycline.

 The invention relates also to a method of detecting
differentially expressed genes correlated with a cancer
25 comprising detecting at least one library of polynucleotide
sequences as above defined or of products encoded by said
library in a sample obtained from a patient.

 A particular embodiment of the invention relates
30 to a polynucleotide library of corresponding substantially to
any combination of at least one polynucleotide sequence
selected among those included in each one of predefined
polynucleotide sequences sets 1 to set 212 as defined in
table 4

The invention relates obviously to polynucleotide libraries comprising at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of said predefined sets, allowing to obtain a discriminating gene pattern, namely to distinguish between normal patients and patients suffering from tumor pathology, between patients having an hormone sensitive tumor and patients having an hormone resistant tumor, between patients having a tumor with lymph nodes from patients having a tumor without lymph nodes, between patients having an antracycline-sensitive tumor from patients having an antracycline-insensitive tumor and between patients having good prognosis primary breast tumors and patients having poor prognosis primary breast tumors.

Polynucleotide sequences library useful for the realization of the invention can comprise also any sequence comprised between 3'end and 5'end of each polynucleotide sequence set as defined in table 4, allowing the complete detection of the implicated genes.

The invention relates also to a polynucleotide library useful to differentiate a normal cell from a cancer cell wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets indicated on table 5, useful in differentiating a normal cell from a cancer cell.

Preferably the polynucleotide library useful to differentiate a normal cell from a cancer cell correspond

substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets indicated on table 5A, and of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets indicated in table 5B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 5A, together with detection of an underexpression of genes identified with sets of polynucleotides sequences defined in table 5B allows to distinguish between normal patients, and patients suffering from tumor pathology.

The invention relates also to a polynucleotide library useful to detect a hormone sensitive tumor cell wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6

Preferably the polynucleotide library useful to detect a hormone sensitive tumor cell correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 6A, together with detection of an underexpression of

genes identified with sets of polynucleotides sequences defined in table 6B allows to distinguish between patients having an hormone sensitive tumor and patients having an hormone resistant tumor.

5

The invention concerns also a polynucleotide library useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7.

Preferably, the polynucleotide library useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 7A, together with detection of an underexpression of genes identified with sets of polynucleotides sequences defined in table 7B allows to distinguish between patients having a tumor with lymph nodes from patients having a tumor without lymph nodes.

The invention concerns also a polynucleotide library useful to differentiate anthracycline-sensitive tumors

from anthracycline-insensitive tumors wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8.

Preferably, the polynucleotide library useful to differentiate anthracycline-sensitive tumors from anthracycline-insensitive tumors correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 8A, together with detection of an underexpression of genes identified with sets of polynucleotides sequences defined in table 8B allows to distinguish between patients having an anthracycline-sensitive tumor from patients having an anthracycline-insensitive tumor.

The invention concerns also a polynucleotide library useful to classify good and poor prognosis primary breast tumors wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9.

Preferably, the polynucleotide library useful to classify good and poor prognosis primary breast tumors correspond substantially to any combination of at least one

polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 9A, together with detection of an underexpression of genes identified with sets of polynucleotides sequences defined in table 9B allows to classify patients having good and poor prognosis primary breast tumors.

In a preferred embodiment, the tumor cell presenting underexpressed or overpressed sequences from the polynucleotide library of the invention are breast tumor cells.

In a particular embodiment the polynucleotides of the polynucleotide library of the present invention are immobilized on a solid support in order to form a polynucleotide array, and said solid support is selected from the group consisting of a nylon membrane, nitrocellulose membrane, glass slide, glass beads, membranes on glass support or a silicon chip.

Another object of the present invention concerns a polynucleotide array useful for prognosis or diagnostic of tumor comprising at least one immobilized polynucleotide library set as previously defined.

Then the invention concerns a polynucleotide array useful to differentiate a normal cell from a cancer cell comprising any combination of at least one polynucleotide sequence selected among those included in each

one of predefined polynucleotide sequences sets indicated on table 5, useful in differentiating a normal cell from a cancer cell.

5 Preferably the polynucleotide array useful to differentiate a normal cell from a cancer cell bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets indicated on table 5A, and of at least one polynucleotide sequence selected among those included in each
10 one of predefined polynucleotide sequences sets indicated in table 5B.

The invention relates also to a polynucleotide array useful to detect a hormone sensitive tumor cell
15 comprising any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6

Preferably the polynucleotide array useful to detect a hormone sensitive tumor cell bears any combination
20 of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in
25 table 6B.

The invention concerns also a polynucleotide array useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes comprising any combination of at
30 least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7.

Preferably, the polynucleotide array useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7B.

The invention concerns also a polynucleotide array useful to differentiate anthracycline-sensitive tumors from anthracycline-insensitive tumors comprising any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8.

Preferably, the polynucleotide array useful to differentiate anthracycline-sensitive tumors from anthracycline-insensitive tumors bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8B.

The invention concerns also a polynucleotide array useful to classify good and poor prognosis primary breast tumors comprising any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9.

Preferably, the polynucleotide array useful to classify good and poor prognosis primary breast tumors bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9B.

The present invention concerns also a method for detecting differentially expressed polynucleotide sequences that are correlated with a cancer, said method comprising:

a) obtaining a polynucleotide sample from a patient; and

b) reacting the sample polynucleotide obtained in step (a) with a probe immobilized on a solid support wherein said probe comprises any of the polynucleotide sequences of the libraries previously defined or an expression product encoded by any of the polynucleotide sequences of the libraries previously defined

c) detecting the reaction product of step (b).

Preferably, the polynucleotide sample obtained at step (a) is labeled before its reaction at step (b) with the probe immobilized on a solid support.

The label of the polynucleotide sample is selected from the group consisting of radioactive, colorimetric, enzymatic, molecular amplification, bioluminescent or fluorescent.

In a particular embodiment the reaction product of step (c) is quantified by further comparison of said reaction product to a control sample.

5 In a first embodiment, the polynucleotide sample isolated from the patient and obtained at step (a) is either RNA or mRNA.

In another embodiment the polynucleotide sample isolated from the patient is cDNA is obtained by reverse transcription of the mRNA.

10 Preferably the reaction step (b) of the method for detecting differentially expressed polynucleotide sequences comprises a hybridization of the sample RNA issued from patient with the probe.

15 Preferably the sample RNA is labeled before hybridization with the probe and the label is selected from the group consisting of radioactive, colorimetric, enzymatic, molecular amplification, bioluminescent or fluorescent.

20 This method for detecting differentially expressed polynucleotide sequences is particularly useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating conditions associated with cancer, and particularly breast cancer.

25 The method for detecting differentially expressed polynucleotide sequences is also particularly useful when the product encoded by any of the polynucleotide sequences or subsequences set is involved in a receptor-ligand reaction on which detection is based.

30 The present invention is also related with a method for screening an anti-tumor agent comprising the method the above-depicted method for detecting differentially expressed polynucleotide sequences wherein the sample has been treated with the anti-tumor agent to be screened.

In a particular embodiment the method for screening an anti-tumor agent comprises detecting polynucleotide sequences reacting with at least one library of polynucleotides or polynucleotide sequences set as previously defined or of products encoded by said library in a sample obtained from a patient.

The invention is illustrated by examples detailed below related to particular experimental results obtained with selected libraries of polypeptides useful to identify and distinguish tumor samples from normal ones.

Tumor samples and RNA extraction

To avoid any bias of selection as to the type and size of the tumors, the RNAs to be tested were prepared from unselected samples. Samples of primary invasive breast carcinomas were collected from 34 patients undergoing surgery at the Institute Paoli-Calmette. After surgical resection, the tumors were macrodissected: a section was taken for the pathologist's diagnosis and an adjacent piece was quickly frozen in liquid nitrogen for molecular analyses. The median age of patients at the time of diagnosis was 55 years (range 39, 83) and most of them were post-menopausal. Tumors were classified according to the WHO histological typing of breast tumors in: 29 ductal carcinomas, 2 lobular carcinomas, 1 mixed ductal and lobular carcinoma, and 2 medullar carcinomas. They had various sizes, inferior or equal to 20 mm (n = 13), between 20 and 50 mm (n = 18) or superior to 50 mm (n = 3), axillary's lymph node status (negative: 19 tumors, positive: 15 tumors), SBR grading (I: 3 tumors, II: 20 tumors, III: 10 tumors, not evaluable: 1 tumor), and estrogen receptor status (ER) evaluated by

immunohistochemical assay (23 ER-positive, 11 ER-negative). ER positivity cutoff value was 10%. Adjuvant treatment with radiotherapy and when necessary multi-agent anthracyclin-based chemotherapy (n = 16) was given to patients according to local practice.

Total RNA was extracted from tumor samples by standard methods (43). Total RNA from normal breast tissue was obtained from Clontech (Palo Alto, CA): RNA was isolated from 8 tissue specimens from Caucasian females, age range 23 - 47. RNA integrity was controlled by denaturing formaldehyde agarose gel electrophoresis and Northern blots using a 28S-specific oligonucleotide.

cDNA arrays preparation

Gene expression was analyzed by hybridization of arrays with radioactive probes. The arrays contained PCR products of 5 control clones, and 180 IMAGE human cDNA clones selected with practical criteria (3' sequence of mRNA, same cloning vector, host bacteria and insert size). This represented 176 genes (4 genes were represented by 2 different clones): 121 with proven or putative implication in cancer and 55 implicated in immune reactions (the list is available on the web site: <http://tagc.univ-mrs.fr/pub/Cancer/>). Their identity was verified by 5' tag-sequencing of plasmid DNA and comparison with sequences in the EST (dbEST) and nucleotide (GenBank) databases at the NCBI. Identity was confirmed for all but 14 clones without significant gene similarity, which were referenced by their GenBank accession number. The control clones were: Arabidopsis thaliana cytochrome c554 gene (used for hybridization signal normalization), 3 poly(A) sequences of different sizes and the vector pT7T3D (negative controls).

PCR amplification, purification and robotical spotting of PCR products onto Hybond-N+ membranes (Amersham) were done according to described protocols (4). All PCR products were spotted in duplicate. For normalization purpose, the c554 gene was spotted 96-fold scattered over the whole membrane.

cDNA array hybridizations

Hybridizations were done successively with a vector oligonucleotide (to precisely determine the amount of target DNA accessible to hybridization in each spot), then after stripping of vector probe, with complex probes made from the RNAs (4). Each complex probe was hybridized to a distinct filter. Probes were prepared from total RNA with an excess of oligo(dT25) to saturate the poly(A) tails of the messengers, and to insure that the reverse transcribed product did not contain long poly(T) sequences. A precise amount of c554 mRNA was added to the total RNA before labeling to allow normalization of the data.

Five ng of total RNA (~100ng of mRNA) from tissue samples were used for each labeling. Probe preparation and hybridization of the membranes were done according to known procedures (<http://tagc.univ-mrs.fr/pub/Cancer/>).

Hybridization was done in excess of target (~15 ng of DNA in each spot) and binding of cDNAs to the targets was linear and proportional to the quantity of cDNA in the probe.

Detection and quantification of cDNA array hybridization signals

Quantitative data were obtained using an imaging plate device. Hybridization signal detection with a FUJI BAS 1500 machine and quantification with the HDG Analyzer

software (Genomic Solutions, Ann Arbor, MI) were done as previously described (<http://tagc.univ-mrs.fr/pub/Cancer/>). Quantification was done by integrating all spot pixel intensities and subtracting a spot background value determined in the neighboring area. Spots were located with a LaPlacian transformation. Spot background level was the median intensity of all the pixels present in a small window centered on the spot and which were not part of any spot (44). Quantified data were normalized in three steps and expressed as absolute gene expression levels (i.e. in percentage of abundance of individual mRNA with respect to mRNA within the sample), as described (4).

Array data analysis

Before analysis of the results, the reproducibility of the experiments was verified by comparing duplicate spots, or one hybridization with the same probe on two independent arrays, or two independent hybridizations with probes prepared from the same RNA. In every case, the results showed good reproducibility with respective correlation coefficients of 0.95, 0.98 and 0.98 (data not shown). Moreover, genes represented by two different clones on the array, such as CDK4 or ETV5, displayed similar expression profiles for the two clones in all samples. This reproducibility was sufficient enough to consider a 2-fold expression difference as significantly differential.

For graphical representation, data were displayed as absolute expression levels (Fig. 2a). For better visualization of clustering, results were log-transformed and displayed as relative values median-centered in each row and in each column (Fig. 2b). Hierarchical clustering was applied to the tissue samples and the genes using the Cluster program developed by Eisen (45) (average linkage clustering

using Pearson correlation as similarity metric). Results in Figs. 2 and 3 were displayed with the TreeView program (45).

Subsequent analysis was done using Excel software (Microsoft) and statistical analyses with the SPSS software. Metastasis-free survival and overall survival were measured from diagnosis until the first metastatic relapse or death respectively. They were estimated with the Kaplan-Meier method and compared between groups with the Log-Rank test. Correlations of gene pairs based on expression profiles were measured with the correlation coefficient r . The search for genes with expression levels correlated with tumor parameters was done in several successive steps.

First, genes were detected by comparing their median expression level in the two subgroups of tumors discordant according to the parameter of interest. The median values rather than the mean values were used because of the high variability of the expression levels for many genes, resulting in a standard deviation of expression level similar or superior to the mean value and making comparisons with means impossible. Second, these detected genes were inspected visually on graphics, and finally, an appropriate statistical analysis was applied to those that were convincing to validate the correlation. Comparison of GATA3 expression between ER-positive tumors and ER-negative tumors was validated using a Mann-Witney test. Correlation coefficients were used to compare the gene expression levels to the number of axillary nodes involved.

Northern blot analysis

Seventy-nine breast tumors, including 22 of the 34 tested on the arrays, were analyzed for GATA3 expression by Northern blot hybridization. RNA extraction from tumor samples and Northern blots were done as previously described

(43). The GATA3 probe was prepared from the IMAGE cDNA clone 129757, which corresponds to the 3' region (from +843 to +1689) of the GATA3 cDNA sequence (GenBank accession no. X55122). The insert (846 bp) was obtained by digestion of the clone with EcoRI and PacI enzymes. Northern blots were stripped and re-hybridized using a α -actin probe (46).

Fig. 1 shows an example of differential gene expression between normal breast tissue (NB) and breast tumor samples. Each cDNA array on Nylon filter was hybridized with a complex probe made from 5 μ g of total RNA. The top image corresponds to the whole membrane. For the two bottom images, only the right portion of the membranes is shown. Numbers below the spots indicate housekeeping genes (1, GAPDH and 2, actin), negative control clones (3, 4 and 5) and examples of genes differentially expressed between NB and breast tumor (6, stromelysin3; 7, ERBB2; 8, MYBL2; 9, FOS; 10, TGF α 3; 11, desmin), and between ER- breast tumor and ER+ breast tumor (12, GATA3).

Fig. 2 is a representation of expression levels of 176 genes in normal breast tissue (NB) and 34 samples of breast carcinoma. Each column corresponds to a single tissue, and each row to a single gene. (a) The results are expressed as percentage abundance of individual mRNA within the sample, and are represented using a blue color scale. The color scale (log scale with a 3-fold interval) indicated at the bottom left ranges from light blue (expression level 0.001%) to dark blue (expression level > 3%). White squares indicate clones with undetectable expression levels and gray squares indicate missing data. The tissue samples are arbitrarily ordered and the clones are ordered from top to bottom according to increasing median expression levels. Horizontal black arrows on the right of the figure mark three clones with highly variable expression levels between the

tumors (stromelysin3, IGF2, GATA3 from top to bottom). (b) The results are shown as relative expression levels (relative to the median value of each row and each column) and are represented with a color scale indicated at the bottom left ranging from 1/100 to 100 fold changes (gray squares: missing data). Eighteen clones with median expression level equal to zero in the 34 tumors are omitted. The clustering program arranges samples (n = 35) along the horizontal axis so that those with the most similar expression profiles are placed adjacent to each other. Similarly, clones (n = 162) are near each other along the vertical axis if they show a strong expression profile correlation across all tissues. The length of the branches of the dendrograms capturing respectively the samples (top) and the clones (left) reflects the similarity of the related elements. Two groups of tumors are separated and color coded: group A (blue) and group B (orange). Horizontal black and horizontal red arrows on the right of the figure respectively mark three genes with highly variable expression levels between the tumors (IGF2, GATA3, stromelysin3 from top to bottom) and four pairs of different clones representing four genes. (c) Zoom representation of group A from Figure 2b, excluding the two outlier tumors at the right. The clustering separates two subgroups of tumors, A1 and A2. The dotted branches correspond to tumors associated with metastatic relapse and death. Follow-up was longer in A2 than in A1 (median 81 months vs 47 for A1).

Fig. 3 is prognostic classification of breast cancer by gene expression profiling showing that gene expression-based tumour classification correlates with clinical outcome. The 12 samples of group A (see figure 2b and 2c) were reclustered using the top 32 differentially expressed genes between A1 and A2 subgroups. Data were displayed as in Fig. 2b and shown with the same color key.

The hierarchical clustering was applied to expression data from the 23 clones, out of 32, of which expression levels presented an at least two-fold change in at least two samples (out of 12). Two subgroups of tumors A1 and A2 are shown as well as two groups of differentially expressed clones. The dotted branches of tumor cluster A1 correspond to samples associated with metastatic relapse and death. Figure 3a shows Two-dimensional representation of hierarchical clustering results shown in figures 2a and 2b. The analysis delineates 4 groups of tumours A, B, C and D. Black squares indicate patients alive at last follow-up visit and red squares indicate patients who died. Three classes of patients with a statistically different clinical outcome were defined according to gene expression profiles: class A (n = 16), class B+C (n = 34), class D (n = 5). Figure 3b illustrates Kaplan-Meier plot of overall survival of the 3 classes of patients ($p < 0.005$, log-rank test). And figure 3c illustrates Kaplan-Meier plot of metastasis-free survival of the 3 classes of patients ($p < 0.05$, log-rank test).

Fig. 4 shows the correlation of GATA3 expression with ER phenotype. (a) The expression levels of GATA3 in 34 breast cancer samples (y axis) monitored by cDNA array analysis are reported in percentage of abundance of individual mRNA with respect to mRNA within the sample (log scale). GATA3 is significantly overexpressed in the ER-positive tumors (n = 23) versus the ER-negative tumors (n = 11) using the Mann-Witney test ($p = 0.0004$). The expression level of GATA3 in normal breast tissue is reported on the right (NB). (b) Northern blot analysis of GATA3 in normal breast sample (NB) and 9 breast cancer samples (AT: tumor analyzed with cDNA array and Northern blot; NT: tumor analyzed with Northern blot). Blots were probed successively

with cDNA from GATA3 (top) and α -actin (bottom). ER status is indicated for each tumor sample.

Data representation

5 Fig. 1 shows examples of hybridizations of cDNA arrays with probes made from RNA extracted from normal breast tissue and breast tumors.

10 The crude results of all hybridizations were processed to be presented either as absolute or relative values in schematic figures. The normalization procedure allowed display of absolute values expressed in percent of abundance of mRNA in the probe as shown in Fig. 2a. Each level of the blue color ladder represents a 3-fold interval of absolute abundance of mRNA. Each column corresponds to a tissue sample and each row to a gene. For graphic purposes, genes were ordered from top to bottom according to increasing median expression levels. Tumor samples were not ordered. The values in each sample displayed a wide range of intensities (3 decades in log scale) corresponding to expression levels ranging from approximately 0.002% to 5% of mRNA abundance. Many genes (see for example stromelysin 3, IGF2 and GATA3, arrows) displayed highly variable expression levels across all tumor samples, scattered over the whole dynamic range of values. A representation of relative values is shown in Fig. 2b. Absolute values were log-transformed, omitting 18 clones whose median intensity was equal to zero across all tissues. Data for each of the 162 remaining clones were then median-centered, as well as data for each sample, so that the relative variation was shown, rather than the absolute intensity. A color scale was used to display data: red for expression level higher than the median and green for expression level lower than the median. The magnitude of the deviation from the median was represented by

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the color intensity. A hierarchical clustering program was then applied to group the 35 samples according to their overall gene expression profiles, and to group the 162 clones on the basis of similarity of their expression levels in all tissues. This resulted in a picture highlighting groups of correlated tissues and groups of correlated genes as depicted by dendrograms.

Breast tumor classification

As shown in Fig. 2b, the clustering algorithm identified two groups of samples, designated A (n = 15, including normal breast, NB) and B (n = 20). These groups were similar with respect to patient age, menopausal status at diagnosis, SBR grading and tumor pathological size. However, 72% of tumors in group A were node-positive and 75% in group B were node-negative. Moreover, 80% of the tumors in group B were estrogen receptor (ER) positive and 50% in group A were ER-negative. With a median follow-up of 44 months after diagnosis, overall survival was different between A and B groups: 5 women died in A (median follow-up 58 months) and 1 in B (median follow-up 40 months). But the frequency of metastatic relapse was relatively similar in the two groups, with 5 women who relapsed in A and 6 in B. Because the time between the diagnosis of metastasis and last follow-up is too short in B, a longer follow-up is needed to determine if these two different groups, defined with expression profiles, have really a different outcome with respect to overall survival.

In the group A of 15 samples, three samples (normal breast and two tumors) were different from each other and from the other 12 samples. The latter constituted two subgroups of tumors, A1 (n = 6) and A2 (n = 6), which could be further separated by clustering as shown in Fig. 2c. The

12 tumors had an uniformly high risk of metastatic relapse according to conventional prognostic features as shown in Table 1. Most of them had received comparable adjuvant anthracyclin-based chemotherapy after surgery, with more women treated in the A1 subgroup. Interestingly, these two subgroups, which could not be distinguished with commonly used histoclinical features, had a very different clinical outcome: there were 4 metastatic relapses and 4 deaths in A1 (median follow-up: 44 months). In contrast and despite a longer median follow-up (90 months), no metastasis or death occurred in A2. This resulted in a significant better metastasis-free survival ($p = 0.01$) and overall survival ($p = 0.005$) for group A2 than for group A1 tumors. No such subgrouping could be done in B.

TABLE 1

Subgroup	A1						A2					
Tumor position in the cluster	1	2	3	4	5	6	7	8	9	10	11	12
Age, years	46	58	60	63	51	58	46	47	50	47	46	66
Nodal status	1	0	0	16	13	37	10	4	1	2	0	0
Histological size, mm	60	20	26	35	20	30	27	25	30	25	20	22
SBR grade	II	III	III	III	III	III	II	II	II	II	II	II
ER status	neg	neg	neg	neg	neg	neg	pos	neg	pos	pos	pos	pos
Adjuvant chemotherapy	yes	yes	no	yes	yes	yes	yes	yes	no	yes	no	no
Metastasis	yes	no	yes	yes	no	yes	no	no	no	no	no	no
Follow-up, months	58	106	35	47	41	31	85	98	95	49	19	141
Patient status	D	A	D	D	A	D	A	A	A	A	A	A

Patient characteristics in subgroups A1 and A2. The 12 tumors are numbered from 1 to 12 according to their position from left to right in the clustering graphic displayed in Fig. 3. Adjuvant chemotherapy was anthracyclin-based. In the line concerning the patient status, A means alive and D means death from cancer progression.

Genes responsible for group A substructure were searched. These are potentially relevant to the prognosis and the sensitivity to chemotherapy in these tumors. Thirty-two genes out of 188 were identified by comparing their median expression level in A1 vs A2. Then, the 12 tumors were reclustered using the expression profiles of these genes as shown in Fig. 3. The same subgroups A1 and A2 were evident and separated by 2 groups of genes: as expected, high expression of ERBB2, MYC and EGFR was associated with bad prognosis subgroup A1 (6-8), and that of E-cadherin and the proto-oncogene MYB with good prognosis subgroup A2 (9, 10). For most of the other genes, these results may stimulate new investigations. Differentiation state is a good prognostic factor in breast cancer and, accordingly, genes associated with cell differentiation, such as GATA3 (11) and CRABP2 (12), had a high level of expression in the better outcome group. The high expression of Ephrin-A1 mRNA in the bad prognosis subgroup suggests a role of this growth factor in breast cancer and can be paralleled with its up-regulation during melanoma progression (13).

Differential gene expression between normal breast and breast tumors

To identify genes differentially expressed between breast tumors (T) and normal breast (NB), the NB value for each gene was compared to its expression level in each tumor. When the expression level of a gene in NB was undetectable, only qualitative information could be deduced and the mRNA was considered as differentially expressed if the signal intensity in the tumor was superior to the reproducibility threshold (0.002% of mRNA abundance). In the other cases, differential expression was defined by an at least 2-fold expression difference. Also, the number of

tumors where it was over- or underexpressed was measured. Table 2 shows a list of the top 20 over- and underexpressed genes. For these genes, the T/NB ratio is reported, where T represented their median expression value in the 34 tumors. This ratio ranged from 2.70 (ABCC5) to 17.76 (GATA3) for the overexpressed genes, and from 0.00 (desmin) to 0.29 (APC) for the underexpressed genes.

TABLE 2

Clone ID	Gene/Protein identity	Gene symbol	Chrom. location	N	T/NB
	Overexpressed genes				
154343	Granzyme H	GZMH	14q11.2	32	9,51
235947	Stromelysin 3	STMY3	22q11.2	31	15,92
207378	MYB Related Protein B	MYBL2	20q13.1	31	(a)
153275	Cellular Retinoic Acid Binding Protein 2	CRABP2	1q21.3	29	7,16
129757	GATA-binding protein 3	GATA3	10p15	28	17,76
120649	T-Lymphocyte surface CD2 antigen	CD2	1p13.1	28	7,54
109677	CREB Binding Protein	CREBBP	16p13.3	28	5,08
172152	EGFR-binding protein GRB2	GRB2	17q24-q25	28	5,00
66969	Transcription factor RELB	RELB	19	28	3,61
182007	ETS-Related Transcription Factor ELF1	ELF1	13q13	27	3,58
153446	LIM domain protein RIL	RIL	5q31.1	26	4,03
203394	ETS Variant gene 5 (ETS-related molecule)	ETV5	3q28	25	3,67
160963	Thrombospondin 1	THBS1	15q15	25	3,39
188393	POU domain, class 2, transcription Factor 2	POU2F2	19	24	4,02

Clone ID	Gene/Protein identity	Gene symbol	Chrom. location	N	T/NB
187822	Integrin, beta 2	ITGB2	21q22.3	24	3,01
243907	Nuclear Factor of Activating T cell Subunit p45	NF45	1	24	2,84
158347	EST H27202	EST		23	2,91
230933	EST AW184517	EST		22	2,85
212366	ATP-Binding Cassette, sub-family C (CFTR/MRP), 5	ABCC5	3q27	22	2,70
149401	Cathepsin D	CTSD	11p15.5	21	2,97
	Underexpressed genes				
153854	Desmin	DES	2q35	34	0,00
208717	P55-C-FOS proto-oncogene protein	FOS	14q24.3	33	0,05
159093	Transcription Factor AP4	TFAP4	16p13	33	0,11
124340	Tenascin XA	TNXA	6p21.3	33	0,14
133738	Prolactin	PRL	6p22.2-p21.3	32	0,00
133891	Chorionic Somatomammotropin Hormone 1	CSH1	17q22-q24	32	0,00
151501	Tyrosine Kinase Receptor TEK	TEK	9p21	32	0,00
183030	Activating Transcription Factor 3	ATF3	1	32	0,07
120916	Phosphodiesterase I	PDNP2	8q24.1	32	0,14
155716	EST R72075	EST		31	0,00
208118	Transforming Growth Factor Beta Receptor Type III	TGFBR3	1p33-p32	31	0,14
187547	Diphtheria Toxin Receptor	DTR	5q23	31	0,17
108490	HIV-1 Rev Binding protein	HRB	2q36	31	0,20
147002	B-cell CLL/lymphoma 2	BCL2	18q21.3	31	0,26
182610	Microsomal Glutathione S Transferase 1	MGST1	12p12.3-p12.1	31	0,28
152802	Phospholipase A2 Membrane	PLA2G2A	1p35	30	0,03

Clone ID	Gene/Protein identity	Gene symbol	Chrom. location	N	T/NB
	Associated, group IIA				
183087	Interleukin 3 Receptor Alpha chain	IL3RA	Xp22.3;Yp13.3	30	0,24
108571	Retinoblastoma-Like 2 (p130)	RBL2	16q12.2	29	0,28
125294	Adenomatous Polyposis Coli Protein	APC	5q21-q22	29	0,29
151767	FASL Receptor	TNFRSF6	10q24.1	28	0,27

List of the genes that show the most frequent differential expression between normal breast tissue and 34 breast carcinomas as measured by cDNA array analysis. N indicates the number of tumor samples where the gene is dysregulated (fold change > 2) compared to normal breast tissue. T/NB represents the ratio: median expression level in 34 breast tumors / expression level in normal breast. (a) MYBL2 transcript displayed a median expression level of 0.025% in breast tumors and was undetectable in NB.

High expression of mucin 1, NM23, ERBB2, FGFR1 and FGFR2, MYC, stromelysin3, cathepsin D and downregulation of FOS, APC, RBL2, FAS, BCL2 were found, reflecting what is known about their biology in cancer. GATA3, which codes for a member of the GATA family of zinc finger transcription factors, and CRABP2, encoding one of the two cellular retinoic acid-binding proteins, showed high expression of mRNA, extending previous results on cDNA arrays (4).

Differential gene expression among various breast tumors and correlation with histoclinical prognostic parameters

To search for potential prognostic markers in breast cancer, genes with expression levels correlated with conventional histoclinical prognostic parameters were looked for: age of patients, axillary node status, tumor size, histological grade and ER status. No significant correlation was found with age, tumor size and histological grade. However, the expression profiles of some genes correlated with ER status and axillary node involvement.

To identify genes potentially relevant to the hormone-responsive phenotype, the gene expression profiles in ER-positive breast cancers (n = 23) vs ER-negative breast cancers (n = 11) were compared. Sixteen clones displayed a median intensity of 0 in both groups. Twenty-five presented a fold change superior to 2. Table 3a displays the top 10 over- and underexpressed genes. Among them, the most differentially expressed was GATA3 with a median intensity ratio ER+/ER- of 28.6 and a value for the first quartile of ER-positive tumors superior (5-fold) to the value of the third quartile of the ER-negative tumors as shown in Fig. 4a. The high expression of GATA3 in ER-positive tumors was statistically significant using a Mann-Witney test (p 0.001). All ER-positive tumors and only 18% of ER-negative tumors displayed a GATA3 expression level greatly superior (fold change > 3) to the normal breast value. Furthermore GATA3 expression was analyzed by Northern blot hybridization (Fig. 4b) in a panel of 79 breast cancers (21 ER-negative tumors and 58 ER-positive tumors), including 22 of the tumors analyzed with cDNA arrays. It confirmed the array results for those 22 tumors as well as the strong correlation between ER status and GATA3 RNA expression (Mann-Witney test, p ≤ 0.0001).

TABLE 3A

Clone ID	Gene/Protein identity	Gene symbol	ER+/ER-
129757	GATA-binding protein 3	GATA3	28,6
356763	Granzyme A	GZMA	5,7
248613	MYB proto-oncogene	MYB	3,4
211999	KIAA1075 protein	KIAA1075	3,3
235947	Stromelysin 3	STMY3	3,1
229839	Macrophage Stimulating 1	MST1	2,8
153275	Cellular Retinoic Acid Binding Protein 2	CRABP2	2,7
301950	X-box Binding Protein 1	XBP1	2,7
205314	Tumor Protein p53	TP53	2,5
126233	Insulin-like Growth Factor 2	IGF2	2,4
66322	CD3G antigen, Gamma	CD3G	0,0
195022	Interleukin 2 Receptor Gamma chain	IL2RG	0,0
111461	SOX4 Protein	SOX4	0,4
151475	Epidermal Growth Factor Receptor	EGFR	0,5
195022	Interleukin 2 Receptor Beta chain	IL2RB	0,5
130788	Topoisomerase (DNA) II beta (180kD)	TOP2B	0,6
323948	SOX9 Protein	SOX9	0,6
183641	S100 calcium-binding protein Beta	S100B	0,6
246620	EST N53133	EST	0,6
231424	Glutathione S Transferase Pi	GSTP1	0,6

To search for genes whose expression profile was correlated with axillary lymph node status, a strong prognostic factor in breast cancer, the group of node-negative tumors (n = 19) was compared with the group of tumors with massive axillary extension (10 or more positive nodes). Furthermore, because survival decreases with the increase of the number of tumor-involved lymph nodes and because the expression measurements were quantitative, it was looked for a correlation between the expression levels of

these genes and the number of tumor-involved nodes (quantitative variables). Table 3b shows a list of the top 10 over- and underexpressed genes between these 2 groups. Most of these genes have not been previously reported as associated with node status, but some of these results are in agreement with literature data. The gene encoding the tyrosine kinase receptor ERBB2 was the most significantly overexpressed gene in node-positive tumors and displayed the highest correlation coefficient ($r = 0.68$; $p \leq 0.0001$).

TABLE 3B

Clone ID	Gene/Protein identity	Gene symbol	N-/10N+
129757	GATA-binding protein 3	GATA3	11,0
160963	Thrombospondin 1	THBS1	6,6
151475	Epidermal Growth Factor Receptor	EGFR	5,4
120916	Phosphodiesterase I	PDNP2	4,9
183030	Activating Transcription Factor 3	ATF3	4,6
211999	KIAA1075 protein	KIAA1075	4,5
110480	Nuclear Factor 1 A-type	NF1A	4,5
182264	P-Selectin	SELP	4,4
356763	Granzyme A	GZMA	4,3
214008	E-cadherin	CDH1	4,0
147016	ERBB2 Receptor Protein-Tyrosine Kinase	ERBB2	0,2
179197	Protein Phosphatase PP2A, 55 kD Subunit	PP2A BR gamma	0,2
231424	Glutathione S Transferase Pi	GSTP1	0,4
111461	SOX4 Protein	SOX4	0,4
195022	Interleukin 2 Receptor Beta chain	IL2RB	0,4
220451	Zinc Finger protein 144	ZNF144	0,5
125413	Mucin 1	MUC1	0,6
290007	CD44 antigen, epithelial form	CD44	0,6
108571	Retinoblastoma-Like 2 (p130)	RBL2	0,7
130788	Topoisomerase (DNA) II Beta (180kD)	TOP2B	0,7

Gene clusters

Gene clustering from Fig. 2b showed groups of genes with correlated expression across samples. When different clones represented the same gene, they were

clustered next to each other (red arrows). Correlation coefficients between gene pairs in the 34 tumors were often high (1% of the 13,041 gene pairs showed a correlation coefficient superior to 0.95 - not shown). An example of highly correlated gene expression is that of BCL2 and RBL2. Such correlated expression, although it has not been described in the literature, probably reflects a common mechanism of regulation for these two genes. Furthermore, these genes also exhibited significant correlated expression with other genes such as PPP2CA, AKT2, PRKCSH or TNFRSF6/FAS. In particular, a striking correlated expression between BCL2 and FAS could be observed ($r = 0.91$; data not shown). The exact meaning of this correlation is unknown, although it may reflect the necessary balance between apoptosis and anti-apoptosis for cell survival.

Although in human cancer the proportion of changes that is reflected at the RNA level is not known, monitoring gene expression patterns appears as a very promising way of increasing the knowledge of the disease. Several different types of cancer have been investigated using cDNA arrays: cervical (14), hepatocellular (15), ovarian (16), colon (17) and renal carcinomas (18), glioblastomas (19), melanomas (20) (21), rhabdomyosarcomas (22), acute leukemias (23) and lymphomas (24). In breast cancer, pioneering studies have yielded the first expression patterns (4, 25-31). They have in particular addressed the important issue of molecular differences in hormone responsive and non-responsive breast tumors. Thus, Yang et al. (28) and Hoch et al. (25) compared expression profiles of breast carcinoma cell lines known to represent these two categories and identified a few genes with differential expression. One of these genes was GATA3. In these studies, cell lines were mostly used and tumor samples were rarely

tested and generally in small numbers. The first study analyzing the expression profiles of a large series of breast cancers was published recently (32), but no correlation with clinical outcome was mentioned.

5 Several interesting points can be made based on the present experimentation. First, the differences in expression patterns among the tumors provided molecular transcriptional evidence of the histoclinical heterogeneity of breast cancer. This diversity was multifactorial, linked
10 to many different genes, highlighting the interest of high throughput analysis in this context. It was possible, with a hierarchical clustering program integrating the expression profiles, to separate normal breast tissue from most tumors and, moreover, to identify two different groups of tumors.
15 Most importantly, two different subgroups of tumors with a very distinct clinical outcome that could not be predicted with classical prognostic factors have been identified by clustering. Indeed, all these tumors had a theoretically bad prognosis as evaluated by current histoclinical tools. All
20 these patients would be at the present time treated with adjuvant chemotherapy, but without the capacity for the physicians to identify patients who will benefit of this treatment and those who will not benefit.

 Gene expression profiles were able to make this
25 discrimination. Such predictive tools have important therapeutic implications. Patients with features of poor prognosis are candidates for other treatment than standard chemotherapy, avoiding loss of time and toxicities related to first-line chemotherapy. These results suggest that the
30 histoclinical category of poor prognosis breast cancer, currently treated with adjuvant anthracyclin-based chemotherapy, groups together at least two molecularly distinct subgroups of tumors with different outcome which

would require distinct chemotherapy regimens. Expression profiles could thus provide a new and more accurate way of classifying breast tumors of poor prognosis and managing patients.

5 Similarly, despite molecular heterogeneity, significant correlations between the expression level of genes (GATA3, ERBB2) and histological tumor parameters were identified. The ER-positivity in breast cancer has been correlated with tumor differentiation, low proliferating
10 rate, favorable prognosis and response to hormonal therapy. The relation between hormone sensitivity of breast cancer and ER status is not perfect, and it is possible that some genes related to ER expression are more important than ER to characterize the hormone sensitive phenotype. These genes
15 could serve as predictive factors to guide the therapy.

GATA3 mRNA expression was highly correlated with ER status. GATA3, which is not estrogen-regulated (25), is a transcription factor that could regulate the expression of genes involved in the ER-positive phenotype. Among the other
20 genes that were found associated with ER status during the experimental work leading to the present invention, some, such as MYB (10), stromelysin 3 (33), and CRABP2 (34), have been previously reported expressed at high levels in ER-positive breast tumors. The higher levels of TP53 mRNA in
25 ER-positive tumors studied were surprising, although in agreement with a recent study (27). Most studies concerning TP53 expression analyzed the protein level rather than the mRNA level, and TP53 protein levels are classically negatively correlated with the ER status (35). The high
30 expression of CRABP2 could be related to the better differentiated status of the ER-positive tumors. The low expression of the three immunity-related genes IL2RB, IL2RG and CD3G may be related to the low lymphoid infiltration in

these well differentiated tumors. ERBB2 high expression in breast cancer has been associated with a poor prognosis and some resistance to hormonal therapy and chemotherapy (36). It is involved in the regulation of cellular differentiation, adhesion, and motility. The motility-enhancing activity of ERBB2 (37) could be responsible for the increased metastatic potential and the unfavorable prognosis of the breast tumors that overexpress ERBB2. The low expression of E-cadherin and thrombospondin 1 in node-positive tumors are consistent with their putative role in different steps of metastatic spread: E-cadherin is an epithelial cell adhesion molecule whose disturbance is a prerequisite for the release of invasive cells in carcinomas (38) and thrombospondin 1 inhibits angiogenesis (39). Similarly, the high expression of the molecule surface antigen Mucin 1 in node-positive tumors (40) can reduce cell-cell interactions facilitating cell detachment and metastasis. CD44, encoding a transmembrane glycoprotein involved in cell adhesion and lymph node homing (41) was expressed at high levels in node-positive tumors as well as GSTP1 (Glutathione-S-Transferase Pi), recently reported associated with increased tumor size (27).

Second, there were a number of genes with highly correlated expression patterns. Gene correlations have already been reported with larger series of genes, essentially under dynamic experimental conditions (42) and recently in steady states (17). Here, correlations were based on expression profiles of a relatively small but selected series of genes and in steady states represented by different breast tumors. Gene correlations are potentially useful tools for cancer research in two ways: i)- they can provide information about the general regulation circuitry of a cancerous cell, allowing the identification of regulatory elements controlling expression networks; ii)- they offer the

possibility of reducing the complexity of the system analyzed by replacing, for example, the intensities of a large number of genes present in a gene cluster by their respective mean intensities.

5 Finally, these results highlight the great potential of cDNA array in cancer research. The gene expression profiles confirmed the heterogeneity of breast cancer, and most importantly allowed us to identify, among a series of poor prognosis breast tumors, two subtypes of the
10 disease not yet recognized with usual histoclinical parameters but with a different clinical outcome after adjuvant chemotherapy. Furthermore, the present invention allows detecting genes of which expression was correlated with classical prognostic factors.

15 Table 4 displays a library of polynucleotides SEQ ID NO :1 to SEQ ID NO : 468 corresponding to a population of polynucleotide sequences underexpressed or overexpressed in cells derived from tumors, more particularly breast tumors,
20 and their respective complements.

TABLE 4

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
HRB	1	hiv-1 rev binding protein	SEQ ID No:1		SEQ ID No:2
GATA1	2	gata-binding protein 1 (globin transcription factor 1)		SEQ ID No:3	SEQ ID No:4
TLK2	3	tousled-like kinase 2		SEQ ID No:5	SEQ ID No:6
EST T81919	4	ests, weakly similar to alu7_human alu subfamily sq sequence contamination warning entry [h.sapiens]	SEQ ID No:7	SEQ ID No:8	
CCND1	5	cyclin d1 (prad1: parathyroid adenomatosis 1)	SEQ ID No:9		SEQ ID No:10
STAT1	6	signal transducer and activator of transcription 1, 91kd		SEQ ID No:11	SEQ ID No:12
FGFR2	7	fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome)	SEQ ID No:13	SEQ ID No:14	SEQ ID No:15
EST T89980	8	ests	SEQ ID No:16		
PPP3CC	9	protein phosphatase 3 (formerly 2b), catalytic subunit, gamma isoform (calcineurin a gamma)	SEQ ID No:17	SEQ ID No:18	SEQ ID No:19
EST T90726	10	ests	SEQ ID No:20	SEQ ID No:21	
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
RNF5	12	ring finger protein 5		SEQ ID No:25	SEQ ID No:26
AXL	13	axl receptor tyrosine kinase	SEQ ID No:27	SEQ ID No:28	SEQ ID No:29
CTSB	14	cathepsin b		SEQ ID No:30	SEQ ID No:31
PPP4C	15	protein phosphatase 4 (formerly x), catalytic subunit	SEQ ID No:32	SEQ ID No:33	SEQ ID No:34
EST T79867	16	ests	SEQ ID No:35		
FGFR4	17	fibroblast growth factor receptor 4	SEQ ID No:36	SEQ ID No:37	SEQ ID No:38
ENPP2	18	ectonucleotide pyrophosphatase/phosphodiesterase 2	SEQ ID No:39	SEQ ID No:40	SEQ ID No:41

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		(autotaxin)			
RELA	19	v-rel avian reticuloendotheliosis viral oncogene homolog a (nuclear factor of kappa light polypeptide gene enhancer in b-cells 3 (p65))	SEQ ID No:42		SEQ ID No:43
ITK	20	il2-inducible t-cell kinase		SEQ ID No:44	SEQ ID No:45
TNXB	21	tenascin xb		SEQ ID No:46	SEQ ID No:47
CSF1	22	colony stimulating factor 1 (macrophage)	SEQ ID No:48	SEQ ID No:49	SEQ ID No:50
VIL2	23	villin 2 (ezrin)	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
APC	24	adenomatosis polyposis coli	SEQ ID No:54	SEQ ID No:55	SEQ ID No:56
MUC1	25	mucin 1, transmembrane		SEQ ID No:57	SEQ ID No:58
IGF2	26	insulin-like growth factor 2 (somatomedin a)	SEQ ID No:59	SEQ ID No:60	SEQ ID No:61
EMR1	27	egf-like module containing, mucin-like, hormone receptor-like sequence 1	SEQ ID No:62	SEQ ID No:63	SEQ ID No:64
KIAA0427	28	kiaa0427 gene product	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
SYK	29	spleen tyrosine kinase	SEQ ID No:68	SEQ ID No:69	SEQ ID No:70
IL7R	30	interleukin 7 receptor		SEQ ID No:71	SEQ ID No:72
MYC	31	v-myc avian myelocytomatosis viral oncogene homolog	SEQ ID No:73	SEQ ID No:74	SEQ ID No:75
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
GRB7	33	growth factor receptor-bound protein 7	SEQ ID No:79	SEQ ID No:80	SEQ ID No:81
TOP2B	34	topoisomerase (dna) ii beta (180kd)		SEQ ID No:82	SEQ ID No:83
CASP4	35	caspase 4, apoptosis-related cysteine protease	SEQ ID No:84		SEQ ID No:85
TIMP2	36	tissue inhibitor of metalloproteinase 2		SEQ ID No:86	SEQ ID No:87
DDT	37	d-dopachrome tautomerase	SEQ ID No:88	SEQ ID No:89	SEQ ID No:90
PRL	38	prolactin	SEQ ID	SEQ ID	SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
			No:91	No:92	No:93
PRLR	39	prolactin receptor	SEQ ID No:94	SEQ ID No:95	SEQ ID No:96
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
GATA3	41	gata-binding protein 3	SEQ ID No:100	SEQ ID No:101	SEQ ID No:78
PGF	42	placental growth factor, vascular endothelial growth factor-related protein		SEQ ID No:102	SEQ ID No:103
UBE3A	43	ubiquitin protein ligase e3a (human papilloma virus e6-associated protein, angelman syndrome)		SEQ ID No:104	SEQ ID No:105
TC21	44	oncogene tc21	SEQ ID No:106	SEQ ID No:107	SEQ ID No:108
TIE	45	tyrosine kinase with immunoglobulin and epidermal growth factor homology domains		SEQ ID No:109	SEQ ID No:110
AMFR	46	autocrine motility factor receptor	SEQ ID No:111	SEQ ID No:112	SEQ ID No:113
EST R81127	47	homo sapiens mrna; cdna dkfzp434c136 (from clone dkfzp434c136)	SEQ ID No:114		
BCL2	48	b-cell cll/lymphoma 2	SEQ ID No:115	SEQ ID No:116	SEQ ID No:117
ERBB2	49	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)		SEQ ID No:118	SEQ ID No:119
MDM2	50	mouse double minute 2, human homolog of; p53-binding protein		SEQ ID No:120	SEQ ID No:121
GATA3	51	gata-binding protein 3	SEQ ID No:122		SEQ ID No:78
HIP-55	52	src homology 3 domain-containing protein hip-55	SEQ ID No:123	SEQ ID No:124	SEQ ID No:125
CTSD	53	cathepsin d (lysosomal aspartyl protease)	SEQ ID No:126	SEQ ID No:127	SEQ ID No:128
IGF1R	54	insulin-like growth factor 1 receptor		SEQ ID No:129	SEQ ID No:130
INSR	55	insulin receptor		SEQ ID No:131	SEQ ID No:132
FOXO1A	56	forkhead box o1a (rhabdomyosarcoma)		SEQ ID No:133	SEQ ID No:134
EGFR	57	epidermal growth factor receptor	SEQ ID	SEQ ID	SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		(avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	No:135	No:136	No:137
TEK	58	tek tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal)	SEQ ID No:138	SEQ ID No:139	SEQ ID No:140
TNFRSF6	59	tumor necrosis factor receptor superfamily, member 6	SEQ ID No:141	SEQ ID No:142	SEQ ID No:143
CDKN1A	60	cyclin-dependent kinase inhibitor 1a (p21, cip1)	SEQ ID No:144	SEQ ID No:145	SEQ ID No:146
PLA2G2A	61	phospholipase a2, group iia (platelets, synovial fluid)	SEQ ID No:147	SEQ ID No:148	SEQ ID No:149
GAPD	62	glyceraldehyde-3-phosphate dehydrogenase	SEQ ID No:150	SEQ ID No:151	SEQ ID No:152
JUNB	63	jun b proto-oncogene	SEQ ID No:153	SEQ ID No:154	SEQ ID No:155
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
ACVRL1	65	activin a receptor type ii-like 1	SEQ ID No:159	SEQ ID No:160	SEQ ID No:161
RIL	66	lim domain protein		SEQ ID No:162	SEQ ID No:163
SHC1	67	shc (src homology 2 domain-containing) transforming protein 1		SEQ ID No:164	SEQ ID No:165
GAPD	68	glyceraldehyde-3-phosphate dehydrogenase	SEQ ID No:166	SEQ ID No:167	SEQ ID No:152
DES	69	desmin	SEQ ID No:168	SEQ ID No:169	SEQ ID No:170
CSNK2B	70	casein kinase 2, beta polypeptide		SEQ ID No:171	SEQ ID No:172
GLG1	71	golgi apparatus protein 1	SEQ ID No:173	SEQ ID No:174	SEQ ID No:175
EDNRB	72	endothelin receptor type b		SEQ ID No:176	SEQ ID No:177
GZMB	73	granzyme b (granzyme 2, cytotoxic t-lymphocyte-associated serine esterase 1)	SEQ ID No:178		SEQ ID No:179
FGFR1	74	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, pfeiffer syndrome)	SEQ ID No:180	SEQ ID No:181	SEQ ID No:182
PPP2CA	75	protein phosphatase 2 (formerly 2a), catalytic subunit, alpha isoform		SEQ ID No:183	SEQ ID No:184
EST R55460	76	homo sapiens, clone image:4054156, mRNA, partial cds		SEQ ID No:185	

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
IGKC	77	immunoglobulin kappa constant	SEQ ID No:186		
MC1R	78	melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor)		SEQ ID No:187	SEQ ID No:188
NRG1	79	neuregulin 1	SEQ ID No:189	SEQ ID No:190	SEQ ID No:191
CNTFR	80	ciliary neurotrophic factor receptor		SEQ ID No:192	SEQ ID No:193
ANG	81	angiogenin, ribonuclease, rnase a family, 5		SEQ ID No:194	SEQ ID No:195
ENG	82	endoglin (osler-rendu-weber syndrome 1)	SEQ ID No:196	SEQ ID No:197	SEQ ID No:198
EGF	83	epidermal growth factor (beta-urogastrone)	SEQ ID No:199		SEQ ID No:200
HRMT1L1	84	hmt1 (hnrnp methyltransferase, s. cerevisiae)-like 1	SEQ ID No:201	SEQ ID No:202	SEQ ID No:203
ETV4	85	ets variant gene 4 (ela enhancer-binding protein, elaf)	SEQ ID No:204	SEQ ID No:205	
ANXA11	86	annexin a11		SEQ ID No:206	SEQ ID No:207
PDGFRB	87	platelet-derived growth factor receptor, beta polypeptide		SEQ ID No:208	SEQ ID No:209
WBSCR14	88	williams-beuren syndrome chromosome region 14		SEQ ID No:210	SEQ ID No:211
CD74	89	cd74 antigen (invariant polypeptide of major histocompatibility complex, class ii antigen-associated)		SEQ ID No:212	SEQ ID No:213
ANXA7	90	annexin a7		SEQ ID No:214	SEQ ID No:215
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
PTPN2	92	protein tyrosine phosphatase, non-receptor type 2	SEQ ID No:218	SEQ ID No:219	SEQ ID No:220
EPHA2	93	epha2	SEQ ID No:221		SEQ ID No:222
TIMP1	94	tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor)	SEQ ID No:223	SEQ ID No:224	SEQ ID No:225
EFNA1	95	ephrin-a1		SEQ ID No:226	SEQ ID No:227

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
EDNRA	96	endothelin receptor type a	SEQ ID No:228		SEQ ID No:229
GRB2	97	growth factor receptor-bound protein 2	SEQ ID No:230	SEQ ID No:231	SEQ ID No:232
JUND	98	jun d proto-oncogene	SEQ ID No:233		SEQ ID No:234
SMARCA2	99	swi/snf related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	SEQ ID No:235	SEQ ID No:236	SEQ ID No:237
PPP2R2C	100	protein phosphatase 2 (formerly 2a), regulatory subunit b (pr 52), gamma isoform	SEQ ID No:238	SEQ ID No:239	
THBS3	101	thrombospondin 3	SEQ ID No:240		SEQ ID No:241
ACTG1	102	actin, gamma 1	SEQ ID No:242	SEQ ID No:243	SEQ ID No:244
ITGA6	103	integrin, alpha 6	SEQ ID No:245	SEQ ID No:246	SEQ ID No:247
RAD9	104	rad9 (s. pombe) homolog	SEQ ID No:248		SEQ ID No:249
ATF3	105	activating transcription factor 3	SEQ ID No:250	SEQ ID No:251	SEQ ID No:252
AKT2	106	v-akt murine thymoma viral oncogene homolog 2	SEQ ID No:253		SEQ ID No:254
S100B	107	s100 calcium-binding protein, beta (neural)		SEQ ID No:255	SEQ ID No:256
ABCB1	108	atp-binding cassette, sub-family b (mdr/tap), member 1	SEQ ID No:257		SEQ ID No:258
SELE	109	selectin e (endothelial adhesion molecule 1)	SEQ ID No:259	SEQ ID No:260	SEQ ID No:261
EGF	110	epidermal growth factor (beta-urogastrone)	SEQ ID No:262		SEQ ID No:200
PRKCSH	111	protein kinase c substrate 80k-h		SEQ ID No:263	SEQ ID No:264
DTR	112	diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor)		SEQ ID No:265	SEQ ID No:266
ITGB2	113	integrin, beta 2 (antigen cd18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit)		SEQ ID No:267	SEQ ID No:268
NEO1	114	neogenin (chicken) homolog 1		SEQ ID No:269	SEQ ID No:270
POU2F2	115	pou domain, class 2, transcription	SEQ ID		SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		factor 2	No:271		No:272
BIRC4	116	baculoviral iap repeat-containing 4	SEQ ID No:273		SEQ ID No:274
DAP3	117	death associated protein 3	SEQ ID No:275		SEQ ID No:276
GNRH1	118	gonadotropin-releasing hormone 1 (leutinizing-releasing hormone)		SEQ ID No:277	SEQ ID No:278
IL2RG	119	interleukin 2 receptor, gamma (severe combined immunodeficiency)	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
DAP3	120	death associated protein 3	SEQ ID No:282	SEQ ID No:283	SEQ ID No:276
PTK2	121	ptk2 protein tyrosine kinase 2		SEQ ID No:284	SEQ ID No:285
CDK4	122	cyclin-dependent kinase 4	SEQ ID No:286	SEQ ID No:287	SEQ ID No:288
BTF3	123	basic transcription factor 3	SEQ ID No:289		SEQ ID No:290
CSF1R	124	colony stimulating factor 1 receptor, formerly mcdonough feline sarcoma viral (v-fms) oncogene homolog	SEQ ID No:291		SEQ ID No:292
FLI1	125	friend leukemia virus integration 1	SEQ ID No:293	SEQ ID No:294	SEQ ID No:295
EST R97218	126	ests, highly similar to tvhume hepatocyte growth factor receptor precursor [h.sapiens]	SEQ ID No:296	SEQ ID No:297	
ETV5	127	ets variant gene 5 (ets-related molecule)	SEQ ID No:298	SEQ ID No:299	SEQ ID No:300
CDK4	128	cyclin-dependent kinase 4	SEQ ID No:301	SEQ ID No:302	SEQ ID No:288
YES1	129	v-yes-1 yamaguchi sarcoma viral oncogene homolog 1	SEQ ID No:303		SEQ ID No:304
IFI75	130	interferon-induced protein 75, 52kd	SEQ ID No:305	SEQ ID No:306	SEQ ID No:307
MYBL2	131	v-myb avian myeloblastosis viral oncogene homolog-like 2	SEQ ID No:308	SEQ ID No:309	SEQ ID No:310
TGFBR3	132	transforming growth factor, beta receptor iii (betaglycan, 300kd)	SEQ ID No:311	SEQ ID No:312	SEQ ID No:313
PRDX2	133	peroxiredoxin 2	SEQ ID No:314	SEQ ID No:315	SEQ ID No:316
FOS	134	v-fos fbj murine osteosarcoma viral oncogene homolog		SEQ ID No:317	SEQ ID No:318

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
RBBP7	135	retinoblastoma-binding protein 7	SEQ ID No:319	SEQ ID No:320	SEQ ID No:321
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
ABCC5	137	atp-binding cassette, sub-family c (cftr/mrp), member 5		SEQ ID No:324	SEQ ID No:325
CDH1	138	cadherin 1, type 1, e-cadherin (epithelial)	SEQ ID No:326	SEQ ID No:327	SEQ ID No:328
ZNF144	139	zinc finger protein 144 (mel-18)		SEQ ID No:329	SEQ ID No:330
MST1	140	macrophage stimulating 1 (hepatocyte growth factor-like)	SEQ ID No:331	SEQ ID No:332	SEQ ID No:333
GSTP1	141	glutathione s-transferase pi	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336
BCL2	142	b-cell cl1/lymphoma 2	SEQ ID No:337	SEQ ID No:338	SEQ ID No:117
PCNA	143	proliferating cell nuclear antigen	SEQ ID No:339	SEQ ID No:340	SEQ ID No:341
BS69	144	adenovirus 5 ela binding protein	SEQ ID No:342	SEQ ID No:343	SEQ ID No:344
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
MGC13071	146	hypothetical protein mgc13071	SEQ ID No:347	SEQ ID No:348	SEQ ID No:349
ILF2	147	interleukin enhancer binding factor 2, 45kd		SEQ ID No:350	SEQ ID No:351
FLJ11307	148	hypothetical protein flj11307	SEQ ID No:352		SEQ ID No:353
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
ZNF9	150	zinc finger protein 9 (a cellular retroviral nucleic acid binding protein)	SEQ ID No:356		SEQ ID No:357
CREM	151	camp responsive element modulator	SEQ ID No:358	SEQ ID No:359	SEQ ID No:360
CTSB	152	cathepsin b	SEQ ID No:361		SEQ ID No:31
MLANA	153	melan-a	SEQ ID No:362	SEQ ID No:363	SEQ ID No:364
APR-1	154	apr-1 protein	SEQ ID No:365	SEQ ID No:366	SEQ ID No:367
ETV5	155	ets variant gene 5 (ets-related	SEQ ID	SEQ ID	SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		molecule)	No:368	No:369	No:300
CD69	156	cd69 antigen (p60, early t-cell activation antigen)		SEQ ID No:370	SEQ ID No:371
TC21	157	oncogene tc21	SEQ ID No:372	SEQ ID No:373	SEQ ID No:108
CD44	158	cd44 antigen (homing function and indian blood group system)	SEQ ID No:374	SEQ ID No:375	SEQ ID No:376
CDKN3	159	cyclin-dependent kinase inhibitor 3 (cdk2-associated dual specificity phosphatase)	SEQ ID No:377	SEQ ID No:378	SEQ ID No:379
MXI1	160	max-interacting protein 1		SEQ ID No:380	SEQ ID No:381
HOXA5	161	homeo box a5	SEQ ID No:382	SEQ ID No:383	SEQ ID No:384
XBP1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
TNFAIP3	163	tumor necrosis factor, alpha-induced protein 3	SEQ ID No:388	SEQ ID No:389	SEQ ID No:390
SRF	164	serum response factor (c-fos serum response element-binding transcription factor)	SEQ ID No:391	SEQ ID No:392	SEQ ID No:393
SOX9	165	sry (sex determining region y)-box 9 (campomelic dysplasia, autosomal sex-reversal)	SEQ ID No:394		SEQ ID No:395
CDH15	166	cadherin 15, m-cadherin (myotubule)	SEQ ID No:396	SEQ ID No:397	SEQ ID No:398
BCL2	167	b-cell cll/lymphoma 2	SEQ ID No:399	SEQ ID No:400	SEQ ID No:117
EST W73386	168	ests	SEQ ID No:401		
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403
FOS	170	v-fos fbj murine osteosarcoma viral oncogene homolog	SEQ ID No:404	SEQ ID No:405	SEQ ID No:318
ILF1	171	interleukin enhancer binding factor 1	SEQ ID No:406	SEQ ID No:407	SEQ ID No:408
ARHGDIA	172	rho gdp dissociation inhibitor (gdi) alpha	SEQ ID No:409	SEQ ID No:410	SEQ ID No:411
C4A	173	complement component 4a	SEQ ID No:412		SEQ ID No:413
CD3G	174	cd3g antigen, gamma polypeptide (tit3 complex)	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
RELB	175	v-rel avian reticuloendotheliosis viral oncogene homolog b (nuclear factor of kappa light polypeptide gene enhancer in b-cells 3)	SEQ ID No:417	SEQ ID No:418	SEQ ID No:419
ESR1	176	estrogen receptor 1	SEQ ID No:420	SEQ ID No:421	SEQ ID No:422
PBX1	177	pre-b-cell leukemia transcription factor 1	SEQ ID No:423	SEQ ID No:424	SEQ ID No:425
GLI3	178	gli-kruppel family member gli3 (greig cephalopolysyndactyly syndrome)	SEQ ID No:426	SEQ ID No:427	SEQ ID No:428
ILF1	179	interleukin enhancer binding factor 1	SEQ ID No:429		SEQ ID No:408
EST T80406	180	similar to SP:S36648 S36648 RB2/P130 PROTEIN	SEQ ID No:430		
EST T95640	181	similar to gb:M16336 T-CELL SURFACE ANTIGEN CD2	SEQ ID No:431		
EST R28523	182	similar to placental lactogen (CSH1)	SEQ ID No:432		
ESTs H21879 & H21880	183	Homo sapiens plasminogen activator (PLAT)	SEQ ID No:433	SEQ ID No:434	
ESTs H24628 & H24592	184	Homo sapiens aminoacylase 1 (ACY1)	SEQ ID No:435	SEQ ID No:436	
EST H28056	185	Homo sapiens E74-like factor 1 (ets domain transcription factor) (ELF1)	SEQ ID No:437		
ESTs H30141 & H27466	186	Homo sapiens selectin P	SEQ ID No:438	SEQ ID No:439	
ESTs H42957 & H42888	187	Human interleukin 3 receptor (hIL-3Ra)	SEQ ID No:440	SEQ ID No:441	
EST H57912	188	Human tumor protein p53 (Li-Fraumeni syndrome) (TP53)	SEQ ID No:442	SEQ ID No:443	
ERBB2	189	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog) (ERBB2)	SEQ ID No:444		
ZNF144	190	zinc finger protein 144 (Mel-18) (ZNF144)	SEQ ID No:445		

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
MARK3	191	MAP/microtubule affinity-regulating kinase 3 (MARK3)	SEQ ID No:446	SEQ ID No:447	
EST N68536	192	EST N68536 MAX-interacting protein 1 (MXI1)	SEQ ID No:448		
EST R81126	193	EST R81126 lymphotoxin beta receptor (LTBR)		SEQ ID No:449	
POU2F2	194	(POU2F2)		SEQ ID No:450	
CASP1	195	caspase 4, apoptosis-related cysteine protease (CASP4) (ex CASP1)		SEQ ID No:451	
HRB	196	syndecan 1 (SDC1) (ex HRB)		SEQ ID No:452	
ITGB2	197	integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit) (ITGB2)	SEQ ID No:453		
MGST1	198	protein phosphatase 1, catalytic subunit, alpha isoform (PPP1CA) (ex MGST1)		SEQ ID No:454	
PPP2CA	199	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform (PPP2CA)	SEQ ID No:455		
SUI1	200	S100 calcium-binding protein A11 (calgizzarin) (S100A11)		SEQ ID No:456	
GZMA	201	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3) (GZMA)		SEQ ID No:457	
EDN1	202	endothelin 1 (EDN1)	SEQ ID No:458		
PTPN6	203	protein tyrosine phosphatase, non-receptor type 6 (PTPN6)	SEQ ID No:459		
TFAP4	204	transcription factor AP-4 (activating enhancer binding protein 4) (TFAP4)	SEQ ID No:460		
CCND2	205	cyclin D2 (CCND2)	SEQ ID No:461		
JUP	206	junction plakoglobin (JUP)	SEQ ID No:462		
GADD45A	207	growth arrest and DNA-damage-inducible, alpha (GADD45A)	SEQ ID No:463		
nm23	208	non-metastatic cells 1, protein (NM23A) expressed in (NME1)	SEQ ID No:464		
BBC1	209	ribosomal protein L13 (RPL13) (ex	SEQ ID		

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		BBC1)	No:465		
VEGFB	210	vascular endothelial growth factor B (VEGFB)	SEQ ID No:466		
LAMR1	211	laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1)	SEQ ID No:467		
CSH1	212	Chorionic somatomammotropin hormone 1 (placental lactogen) = LACTOGEN Precursor		SEQ ID No:468	

Tables 5A and 5B hereunder displays two subpopulations corresponding to the 5 top overexpressed and to the 5 top underexpressed polynucleotide sequences particularly interesting to distinguish healthy person from cancer patient.

TABLE 5A

overexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
GZMB	73	granzyme b (granzyme 2, cytotoxic t-lymphocyte-associated serine esterase 1)	SEQ ID No:178		SEQ ID No:179
MYBL2	131	v-myb avian myeloblastosis viral oncogene homolog-like 2	SEQ ID No:308	SEQ ID No:309	SEQ ID No:310
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
EST T95640	181	similar to gb:M16336 T-CELL SURFACE ANTIGEN CD2	SEQ ID No:431		

TABLE 5B
underexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
PRL	38	prolactin	SEQ ID No:91	SEQ ID No:92	SEQ ID No:93
TEK	58	tek tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal)	SEQ ID No:138	SEQ ID No:139	SEQ ID No:140
PLA2G2A	61	phospholipase a2, group iia (platelets, synovial fluid)	SEQ ID No:147	SEQ ID No:148	SEQ ID No:149
DES	69	desmin	SEQ ID No:168	SEQ ID No:169	SEQ ID No:170
EST R28523	182	similar to placental lactogen (CSH1)	SEQ ID No:432		

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Table 6 hereunder relate to sub populations of polynucleotide sequences interesting to detect hormone sensitive tumors allowing to distinguish between ER+ and ER-samples.

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TABLE 6

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
IGF2	26	insulin-like growth factor 2 (somatomedin a)	SEQ ID No:59	SEQ ID No:60	SEQ ID No:61
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
TOP2B	34	topoisomerase (dna) ii beta (180kd)		SEQ ID No:82	SEQ ID No:83
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
S100B	107	s100 calcium-binding protein, beta (neural)		SEQ ID No:255	SEQ ID No:256
IL2RG	119	interleukin 2 receptor, gamma (severe combined immunodeficiency)	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
MST1	140	macrophage stimulating 1 (hepatocyte growth factor-like)	SEQ ID No:331	SEQ ID No:332	SEQ ID No:333
GSTP1	141	glutathione s-transferase pi	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336
MMP11	145	matrix metalloproteinase (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
FLJ11307	148	hypothetical protein flj11307	SEQ ID No:352		SEQ ID No:353
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
XBP1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
SOX9	165	sry (sex determining region y)-box 9 (campomelic dysplasia, autosomal sex-reversal)	SEQ ID No:394		SEQ ID No:395
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403
CD3G	174	cd3g antigen, gamma polypeptide (tit3 complex)	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416
EST H57912	188	Human tumor protein p53 (Li-Fraumeni syndrome) (TP53)	SEQ ID No:442		

Tables 6A et 6B hereunder relate to two sub populations of polynucleotide sequences particularly interesting to detect hormone sensitive tumors allowing to distinguish between ER+ and ER- samples

Table 6A

overexpressed genes : top 5

ER + / ER -

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403

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Table 6B

underexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
IL2RG	119	interleukin 2 receptor, gamma (severe combined immunodeficiency)	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
CD3G	174	cd3g antigen, gamma polypeptide (tit3 complex)	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416

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Tables 7 hereunder relates to subpopulations of polynucleotide sequences interesting to distinguish tumors with lymph node from tumors with no lymph node.

TABLE 7

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
EST T89980	8	ests	SEQ ID No:16		
SOX4	11	ery (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
ENPP2	18	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	SEQ ID No:39	SEQ ID No:40	SEQ ID No:41
MUC1	25	mucin 1, transmembrane		SEQ ID No:57	SEQ ID No:58
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
TOP2B	34	topoisomerase (dna) ii beta (180kd)		SEQ ID No:82	SEQ ID No:83
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
ERBB2	49	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)		SEQ ID No:118	SEQ ID No:119
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
PPP2R2C	100	protein phosphatase 2 (formerly 2a), regulatory subunit b (pr 52), gamma isoform	SEQ ID No:238	SEQ ID No:239	
ATF3	105	activating transcription factor 3	SEQ ID No:250	SEQ ID No:251	SEQ ID No:252
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
CDH1	138	cadherin 1, type 1, e-cadherin (epithelial)	SEQ ID No:326	SEQ ID No:327	SEQ ID No:328
ZNF144	139	zinc finger protein 144 (mel-18)		SEQ ID No:329	SEQ ID No:330
GSTP1	141	glutathione s-transferase pi	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336
CD44	158	cd44 antigen (homing function and indian blood group system)	SEQ ID No:374	SEQ ID No:375	SEQ ID No:376
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
EST T80406	180	similar to SP:S36648 S36648 RB2/P130 PROTEIN	SEQ ID No:430		
ESTs H30141 & H27466	186	Homo sapiens selectin P	SEQ ID No:438	SEQ ID No:439	

Tables 7A and 7B hereunder relate to two sub populations of polynucleotide sequences particularly interesting to distinguish tumors with lymph node from tumors with no lymph node.

TABLE 7A

Overexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
ENPP2	18	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	SEQ ID No:39	SEQ ID No:40	SEQ ID No:41
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
ATF3	105	activating transcription factor 3	SEQ ID No:250	SEQ ID No:251	SEQ ID No:252

TABLE 7B

Underexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region Y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
ERBB2	49	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)		SEQ ID No:118	SEQ ID No:119
PPP2R2C	100	protein phosphatase 2 (formerly 2a), regulatory subunit b (pr 52), gamma isoform	SEQ ID No:238	SEQ ID No:239	
GSTP1	141	glutathione s-transferase pi	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336

Tables 8, 8A and 8B hereunder relates to sub populations of polynucleotide sequences particularly interesting to distinguish tumors sensitive to antracycline from tumors unsensitive to antracycline.

TABLE 8

A1 /A2

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
CSF1	22	colony stimulating factor 1 (macrophage)	SEQ ID No:48	SEQ ID No:49	SEQ ID No:50
VIL2	23	villin 2 (ezrin)	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
IGF2	26	insulin-like growth factor 2 (somatomedin a)	SEQ ID No:59	SEQ ID No:60	SEQ ID No:61
KIAA0427	28	kiaa0427 gene product	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
MYC	31	v-myc avian myelocytomatosis viral oncogene homolog	SEQ ID No:73	SEQ ID No:74	SEQ ID No:75
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
TOP2B	34	topoisomerase (dna) ii beta (180kd)		SEQ ID No:82	SEQ ID No:83
ERBB2	49	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)		SEQ ID No:118	SEQ ID No:119
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
GZMB	73	granzyme b (granzyme 2, cytotoxic t-lymphocyte-associated serine esterase 1)	SEQ ID No:178		SEQ ID No:179
IGKC	77	immunoglobulin kappa constant	SEQ ID No:186		
ANG	81	angiogenin, ribonuclease, rnase a family, 5		SEQ ID No:194	SEQ ID No:195
EFNA1	95	ephrin-a1		SEQ ID No:226	SEQ ID No:227
MYBL2	131	v-myb avian myeloblastosis viral oncogene homolog-like 2	SEQ ID No:308	SEQ ID No:309	SEQ ID No:310
CDH1	138	cadherin 1, type 1, e-cadherin (epithelial)	SEQ ID No:326	SEQ ID No:327	SEQ ID No:328
MST1	140	macrophage stimulating 1 (hepatocyte growth factor-like)	SEQ ID No:331	SEQ ID No:332	SEQ ID No:333
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
XBP1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
SRF	164	serum response factor (c-fos serum response element-binding transcription factor)	SEQ ID No:391	SEQ ID No:392	SEQ ID No:393
SOX9	165	sry (sex determining region y)-box 9 (campomelic dysplasia, autosomal sex-reversal)	SEQ ID No:394		SEQ ID No:395
ESTs H21879 & H21880	183	Homo sapiens plasminogen activator (PLAT)	SEQ ID No:433	SEQ ID No:434	

Tables 8A and 8B hereunder relate to two sub populations of polynucleotide sequences particularly interesting to distinguish tumors sensitive to antracycline from tumors unsensitive to antracycline.

TABLEAU 8A

overexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403

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TABLEAU 8B

underexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
IL2RG	119	interleukin 2 receptor, gamma (severe combined immunodeficiency)	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
CD3G	174	cd3g antigen, gamma polypeptide (tit3 complex)	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416

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Tables 9, 9A and 9B hereunder relates to sub populations of polynucleotide sequences particularly interesting in classifying good and poor prognosis primary breast tumors.

TABLE 9

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
CTSB	14	cathepsin b		SEQ ID No:30	SEQ ID No:31
VIL2	23	villin 2 (ezrin)	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
MUC1	25	mucin 1, transmembrane		SEQ ID No:57	SEQ ID No:58
EMR1	27	egf-like module containing, mucin-like, hormone receptor-like sequence 1	SEQ ID No:62	SEQ ID No:63	SEQ ID No:64
KIAA0427	28	kiaa0427 gene product	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
PRLR	39	prolactin receptor	SEQ ID No:94	SEQ ID No:95	SEQ ID No:96
GATA3	41	gata-binding protein 3	SEQ ID No:100	SEQ ID No:101	SEQ ID No:78
TC21	44	oncogene tc21	SEQ ID No:106	SEQ ID No:107	SEQ ID No:108
BCL2	48	b-cell cl1/lymphoma 2	SEQ ID No:115	SEQ ID No:116	SEQ ID No:117
GATA3	51	gata-binding protein 3	SEQ ID No:122		SEQ ID No:78
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
ANG	81	angiogenin, ribonuclease, rnase a family, 5		SEQ ID No:194	SEQ ID No:195
EGF	83	epidermal growth factor (beta-urogastrone)	SEQ ID No:199		SEQ ID No:200
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
EDNRA	96	endothelin receptor type a	SEQ ID No:228		SEQ ID No:229
SMARCA2	99	swi/snf related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	SEQ ID No:235	SEQ ID No:236	SEQ ID No:237
ABCB1	108	atp-binding cassette, sub-family b (mdr/tap), member 1	SEQ ID No:257		SEQ ID No:258
EGF	110	epidermal growth factor (beta-urogastrone)	SEQ ID No:262		SEQ ID No:200
BIRC4	116	baculoviral iap repeat-containing 4	SEQ ID No:273		SEQ ID No:274
DAP3	117	death associated protein 3	SEQ ID		SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
			No:275		No:276
GNRH1	118	gonadotropin-releasing hormone 1 (leutinizing-releasing hormone)		SEQ ID No:277	SEQ ID No:278
DAP3	120	death associated protein 3	SEQ ID No:282	SEQ ID No:283	SEQ ID No:276
EST R97218	126	ests, highly similar to tvhume hepatocyte growth factor receptor precursor [h.sapiens]	SEQ ID No:296	SEQ ID No:297	
BCL2	142	b-cell cl1/lymphoma 2	SEQ ID No:337	SEQ ID No:338	SEQ ID No:117
BS69	144	adenovirus 5 ela binding protein	SEQ ID No:342	SEQ ID No:343	SEQ ID No:344
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
CTSB	152	cathepsin b	SEQ ID No:361		SEQ ID No:31
MLANA	153	melan-a	SEQ ID No:362	SEQ ID No:363	SEQ ID No:364
APR-1	154	apr-1 protein	SEQ ID No:365	SEQ ID No:366	SEQ ID No:367
TC21	157	oncogene tc21	SEQ ID No:372	SEQ ID No:373	SEQ ID No:108
CDKN3	159	cyclin-dependent kinase inhibitor 3 (cdk2-associated dual specificity phosphatase)	SEQ ID No:377	SEQ ID No:378	SEQ ID No:379
XBP1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
CDH15	166	cadherin 15, m-cadherin (myotubule)	SEQ ID No:396	SEQ ID No:397	SEQ ID No:398
BCL2	167	b-cell cl1/lymphoma 2	SEQ ID No:399	SEQ ID No:400	SEQ ID No:117
EST W73386	168	ests	SEQ ID No:401		
ILF1	171	interleukin enhancer binding factor 1	SEQ ID No:406	SEQ ID No:407	SEQ ID No:408
ARHGDIA	172	rho gdp dissociation inhibitor (gdi) alpha	SEQ ID No:409	SEQ ID No:410	SEQ ID No:411
C4A	173	complement component 4a	SEQ ID No:412		SEQ ID No:413
ESR1	176	estrogen receptor 1	SEQ ID No:420	SEQ ID No:421	SEQ ID No:422
PBX1	177	pre-b-cell leukemia transcription factor 1	SEQ ID No:423	SEQ ID No:424	SEQ ID No:425
GLI3	178	gli-kruppel family member gli3 (greig	SEQ ID No:426	SEQ ID No:427	SEQ ID No:428

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		cephalopolysyndactyly syndrome)			
ILF1	179	interleukin enhancer binding factor 1	SEQ ID No:429		SEQ ID No:408
ESTs H24628 & H24592	184	Homo sapiens aminoacylase 1 (ACY1).	SEQ ID No:435	SEQ ID No:436	
EST H28056	185	Homo sapiens E74-like factor 1 (ets domain transcription factor) (ELF1)	SEQ ID No:437		

TABLE 9A

Gene symbol	SET N°	Name	Seq3'	Seq5'	Ref
VIL2	23	villin 2 (ezrin)	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
MUC1	25	mucin 1, transmembrane		SEQ ID No:57	SEQ ID No:58
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
GATA3	41	gata-binding protein 3	SEQ ID No:100	SEQ ID No:101	SEQ ID No:78
BCL2	48	b-cell cll/lymphoma 2	SEQ ID No:115	SEQ ID No:116	SEQ ID No:117
GATA3	51	gata-binding protein 3	SEQ ID No:122		SEQ ID No:78
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
ANG	81	angiogenin, ribonuclease, rnase a family, 5		SEQ ID No:194	SEQ ID No:195
EGF	83	epidermal growth factor (beta-urogastrone)	SEQ ID No:199		SEQ ID No:200
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
SMARCA2	99	swi/snf related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	SEQ ID No:235	SEQ ID No:236	SEQ ID No:237
EGF	110	epidermal growth factor (beta-urogastrone)	SEQ ID No:262		SEQ ID No:200
BIRC4	116	baculoviral iap repeat-containing 4	SEQ ID No:273		SEQ ID No:274
BCL2	142	b-cell cll/lymphoma 2	SEQ ID No:337	SEQ ID No:338	SEQ ID No:117

Gene symbol	SET N°	Name	Seq3'	Seq5'	Ref
BS69	144	adenovirus 5 ela binding protein	SEQ ID No:342	SEQ ID No:343	SEQ ID No:344
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
XBP1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
BCL2	167	b-cell cll/lymphoma 2	SEQ ID No:399	SEQ ID No:400	SEQ ID No:117
ILF1	171	interleukin enhancer binding factor 1	SEQ ID No:406	SEQ ID No:407	SEQ ID No:408
ARHGDI A	172	rho gdp dissociation inhibitor (gdi) alpha	SEQ ID No:409	SEQ ID No:410	SEQ ID No:411
C4A	173	complement component 4a	SEQ ID No:412		SEQ ID No:413
ESR1	176	estrogen receptor 1	SEQ ID No:420	SEQ ID No:421	SEQ ID No:422
PBX1	177	pre-b-cell leukemia transcription factor 1	SEQ ID No:423	SEQ ID No:424	SEQ ID No:425
GLI3	178	gli-kruppel family member gli3 (greig cephalopolysyndactyly syndrome)	SEQ ID No:426	SEQ ID No:427	SEQ ID No:428
ILF1	179	interleukin enhancer binding factor 1	SEQ ID No:429		SEQ ID No:408
ESTs H24628 & H24592	184	Homo sapiens aminoacylase 1 (ACY1).	SEQ ID No:435	SEQ ID No:436	
EST H28056	185	Homo sapiens E74-like factor 1 (ets domain transcription factor) (ELF1)	SEQ ID No:437		

TABLE 9B

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
CTSB	14	cathepsin b		SEQ ID No:30	SEQ ID No:31
EMR1	27	egf-like module containing, mucin-like, hormone receptor-like sequence 1	SEQ ID No:62	SEQ ID No:63	SEQ ID No:64
KIAA0427	28	kiaa0427 gene product	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
PRLR	39	prolactin receptor	SEQ ID No:94	SEQ ID No:95	SEQ ID No:96
TC21	44	oncogene tc21	SEQ ID No:106	SEQ ID No:107	SEQ ID No:108

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
EDNRA	96	endothelin receptor type a	SEQ ID No:228		SEQ ID No:229
ABCB1	108	atp-binding cassette, sub-family b (mdr/tap), member 1	SEQ ID No:257		SEQ ID No:258
DAP3	117	death associated protein 3	SEQ ID No:275		SEQ ID No:276
GNRH1	118	gonadotropin-releasing hormone 1 (leutinizing-releasing hormone)		SEQ ID No:277	SEQ ID No:278
DAP3	120	death associated protein 3	SEQ ID No:282	SEQ ID No:283	SEQ ID No:276
EST R97218	126	ests, highly similar to tvhume hepatocyte growth factor receptor precursor [h.sapiens]	SEQ ID No:296	SEQ ID No:297	
CTSB	152	cathepsin b	SEQ ID No:361		SEQ ID No:31
MLANA	153	melan-a	SEQ ID No:362	SEQ ID No:363	SEQ ID No:364
APR-1	154	apr-1 protein	SEQ ID No:365	SEQ ID No:366	SEQ ID No:367
TC21	157	oncogene tc21	SEQ ID No:372	SEQ ID No:373	SEQ ID No:108
CDKN3	159	cyclin-dependent kinase inhibitor 3 (cdk2-associated dual specificity phosphatase)	SEQ ID No:377	SEQ ID No:378	SEQ ID No:379
CDH15	166	cadherin 15, m-cadherin (myotubule)	SEQ ID No:396	SEQ ID No:397	SEQ ID No:398
EST W73386	168	ests	SEQ ID No:401		

Overexpression of genes detected by using at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences indicated in table 9A combined with underexpression of genes detected with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequence indicated on table 9B present a Good outcome.

So, a preferred DNA array according to the invention comprises at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences indicated in table 9A and at least

one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequence indicated on table 9B.

5 Such DNA arrays are particularly useful to distinguish patients having a high risk (Bad Outcome) from those having a good pronostic (Good Outcome).

TABLE 10

CORRELATION BETWEEN SEQ ID NO AS FILED WITH US PROVISIONAL APPLICATION N° 60/254,090
and SEQ ID NO FILED WITH PCT APPLICATION

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
GATA3	1	GATA-binding protein 3 (GATA3)	129757	SEQ ID No : 1		SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
MYB	2	v-myb avian myeloblastosis viral oncogene homolog (MYB)	248613		SEQ ID No : 2	0	SEQ ID No:354	SEQ ID No:355
KIAA1075	3	KIAA1075 protein	211999	SEQ ID No : 3	SEQ ID No : 4	SEQ ID No:322	SEQ ID No:323	0
STMY3	4	matrix metalloproteinase 11 (stromelysin 3) (MMP11) (ex STMY3)	235947	SEQ ID No : 5		SEQ ID No:345	0	SEQ ID No:346
HGFL	5	macrophage-stimulating protein (MST1) (ex HGFL)	229839	SEQ ID No : 6	SEQ ID No : 7	SEQ ID No:331	SEQ ID No:332	SEQ ID No:333
CRABP	6	cellular retinoic acid-binding protein 2 (CRABP2)	153275	SEQ ID No : 8	SEQ ID No : 9	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
XBP1	7	X-box binding protein 1 (XBP1)	301950	SEQ ID No : 10	SEQ ID No : 11	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
TP53	8	tumor protein p53 (LI-Fraumeni syndrome) (TP53)	205314		SEQ ID No : 12	SEQ ID No:442	0	0
IGF2	9	insulin-like growth factor 2 (somatomedin A) (IGF2)	126233	SEQ ID No : 13	SEQ ID No : 14	SEQ ID No:59	SEQ ID No:60	SEQ ID No:61
CD3G	10	CD3G antigen, gamma polypeptide (TIT3 complex)(CD3G)	66322	SEQ ID No : 15	SEQ ID No : 16	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416
IL2RG	11	interleukin 2 receptor, gamma (severe combined immunodeficiency)(IL2RG)	195022	SEQ ID No : 17	SEQ ID No : 18	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
SOX4	12	SRY (sex determining region Y)-box 4 (SOX4)	111461	SEQ ID No : 19	SEQ ID No : 20	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
EGFR	13	epidermal growth factor receptor (avian erythroblastic)	151475	SEQ ID No : 21	SEQ ID No : 22	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
TOP2B	14	topIIb mRNA for topoisomerase IIb.	130788		SEQ ID No : 23	0	SEQ ID No:82	SEQ ID No:83
S100B	15	S100 calcium-binding protein, beta (neural) (S100B)	183641		SEQ ID No : 24	0	SEQ ID No:255	SEQ ID No:256
EST N53133	16	EST N53133	246620	SEQ ID No : 25		SEQ ID No:352	0	SEQ ID No:353
GSTP1	17	glutathione S-transferase pl (GSTP1)	231424	SEQ ID No : 26	SEQ ID No : 27	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336
THBS1	18	thrombospondin 1 (THBS1)	160963	SEQ ID No : 28		SEQ ID No:216	0	SEQ ID No:217

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
PDNIP2	19	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin) (ENPP2) (ex PDNIP2)	120916	SEQ ID No : 29	SEQ ID No : 30	SEQ ID No:39	SEQ ID No:40	SEQ ID No:41
ATF3	20	activating transcription factor 3 (ATF3)	183030	SEQ ID No : 31	SEQ ID No : 32	SEQ ID No:250	SEQ ID No:251	SEQ ID No:252
NF1A	21	(ex NF1A)	110480	SEQ ID No : 33		SEQ ID No:16	0	0
SELP	22	selectin P (granule membrane protein 140kD, antigen CD62) (SELP)	182264		SEQ ID No : 34	SEQ ID No:438	SEQ ID No:439	0
CDH1	23	cadherin 1, E-cadherin (epithelial) (CDH1)	214008	SEQ ID No : 35	SEQ ID No : 36	SEQ ID No:326	SEQ ID No:327	SEQ ID No:328
ERBB2	24	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog) (ERBB2)	147016	SEQ ID No : 37		0	SEQ ID No:118	SEQ ID No:119
PP2A BR gamma	25	(PP2A BR gamma)	179197	SEQ ID No : 38	SEQ ID No : 39	SEQ ID No:238	SEQ ID No:239	0
ZNF144	26	zinc finger protein 144 (Mel-18) (ZNF144)	220451	SEQ ID No : 40	SEQ ID No : 41	0	SEQ ID No:329	SEQ ID No:330
MUC1	27	mucin 1, transmembrane (MUC1)	125413		SEQ ID No : 42	0	SEQ ID No:57	SEQ ID No:58
CD44	28	CD44E (epithelial form)	290007	SEQ ID No : 43	SEQ ID No : 44	SEQ ID No:374	SEQ ID No:375	SEQ ID No:376
PLA2G2A	29	phospholipase A2, group IIA (platelets, synovial fluid) (PLA2G2A), nuclear gene encoding mitochondrial protein	152802	SEQ ID No : 45	SEQ ID No : 46	SEQ ID No:147	SEQ ID No:148	SEQ ID No:149
ACVRL1	30	activin A receptor type II-like 1 (ACVRL1)	153350	SEQ ID No : 47	SEQ ID No : 48	SEQ ID No:159	SEQ ID No:160	SEQ ID No:161
AXL	31	AXL receptor tyrosine kinase (AXL)	112500	SEQ ID No : 49	SEQ ID No : 50	SEQ ID No:27	SEQ ID No:28	SEQ ID No:29
PKU-ALPHA	32	KU-alpha, partial cds (new gene symbol Ttk2)	109569		SEQ ID No : 51	0	SEQ ID No:5	SEQ ID No:6
ABCC5	33	ATP-binding cassette, sub-family C (CFTR/MRP), member 5 (ABCC5)	212366		SEQ ID No : 52	0	SEQ ID No:324	SEQ ID No:325
EDNRB	34	endothelin receptor type B (EDNRB), transcript variant1	154244		SEQ ID No : 53	0	SEQ ID No:176	SEQ ID No:177
DTR	35	diphtheria toxin receptor (heparin-binding epidermal)	187547		SEQ ID No : 54	0	SEQ ID No:265	SEQ ID No:266
IGF1R	36	insulin-like growth factor 1 receptor (IGF1R)	150361		SEQ ID No : 55	0	SEQ ID No:129	SEQ ID No:130
KIAA0427	37	KIAA0427	127507	SEQ ID No : 56	SEQ ID No : 57	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
CD69	38	CD69 antigen (p60, early T-cell activation antigen)	276727		SEQ ID No : 58	0	SEQ ID No:370	SEQ ID No:371
FGFR4	39	fibroblast growth factor receptor 4 (FGFR4)	116781	SEQ ID No : 59	SEQ ID No : 60	SEQ ID No:36	SEQ ID No:37	SEQ ID No:38
EST T85683	40	EST T85683 cathepsin B (CTSB)	112622		SEQ ID No : 61	0	SEQ ID No:30	SEQ ID No:31
EST R00569	41	EST R00569 IL2-Inducible T-cell kinase (ITK)	123871		SEQ ID No : 62	0	SEQ ID No:44	SEQ ID No:45

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
TGFR3	42	transforming growth factor, beta receptor III (TGFR3)	208118	SEQ ID No : 63	SEQ ID No : 64	SEQ ID No:311	SEQ ID No:312	SEQ ID No:313
INSR	43	insulin receptor (INSR)	151149		SEQ ID No : 65	0	SEQ ID No:131	SEQ ID No:132
MARK3	44	MAP/microtubule affinity-regulating kinase 3 (MARK3)	110599	SEQ ID No : 66	SEQ ID No : 67	#N/A	#N/A	#N/A
TIMP2	45	tissue inhibitor of metalloproteinase 2 (TIMP2)	131504		SEQ ID No : 68	0	SEQ ID No:86	SEQ ID No:87
EST R85557	46	EST R85557 thrombospondin 3 (THBS3)	180219	SEQ ID No : 69		SEQ ID No:240	0	SEQ ID No:241
GNRH1	47	gonadotropin-releasing hormone 1 (GNRH1)	192688		SEQ ID No : 70	0	SEQ ID No:277	SEQ ID No:278
FGFR2	48	fibroblast growth factor receptor 2 (FGFR2)	110387	SEQ ID No : 71	SEQ ID No : 72	SEQ ID No:13	SEQ ID No:14	SEQ ID No:15
NFKB2	49	NFKB2	114879	SEQ ID No : 73		SEQ ID No:35	0	0
VIL2	50	villin 2 (ezrin) (VIL2)	124701	SEQ ID No : 74	SEQ ID No : 75	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
ENG	51	endoglin (ENG)	156979	SEQ ID No : 76	SEQ ID No : 77	SEQ ID No:196	SEQ ID No:197	SEQ ID No:198
EPHA2	52	EphA2 (EPHA2)	162004	SEQ ID No : 78		SEQ ID No:221	0	SEQ ID No:222
CREM	53	cAMP responsive element modulator (CREM)	258584	SEQ ID No : 79	SEQ ID No : 80	SEQ ID No:358	SEQ ID No:359	SEQ ID No:360
ETV5-a	54	ets variant gene 5 (ETV5)	270549	SEQ ID No : 81	SEQ ID No : 82	SEQ ID No:368	SEQ ID No:369	SEQ ID No:300
EST N68536	55	EST N68536 MAX-interacting protein 1 (MXI1)	298242	SEQ ID No : 83	SEQ ID No : 84	0	SEQ ID No:380	SEQ ID No:381
EST R81126	56	EST R81126 lymphotoxin beta receptor (LTBR)	146635	SEQ ID No : 85	SEQ ID No : 86	SEQ ID No:114	0	0
POU2F2	57	(POU2F2)	188393	SEQ ID No : 87	SEQ ID No : 88	SEQ ID No:271	0	SEQ ID No:272
FLI1	58	Friend leukemia virus integration 1 (FLI1)	198144	SEQ ID No : 89	SEQ ID No : 90	SEQ ID No:293	SEQ ID No:294	SEQ ID No:295
TIE	59	tyrosine kinase with immunoglobulin and epidermal growth factor homology domains (TIE)	144081		SEQ ID No : 91	0	SEQ ID No:109	SEQ ID No:110
PRLR	60	prolactin receptor (PRLR)	138788	SEQ ID No : 92	SEQ ID No : 93	SEQ ID No:94	SEQ ID No:95	SEQ ID No:96
PPP3CA	61	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma) (PPP3CC) (ex PPP3CA)	110481	SEQ ID No : 94	SEQ ID No : 95	SEQ ID No:17	SEQ ID No:18	SEQ ID No:19
PTPN2	62	protein tyrosine phosphatase, non-receptor type 2 (PTPN2)	161451	SEQ ID No : 96	SEQ ID No : 97	SEQ ID No:218	SEQ ID No:219	SEQ ID No:220
PGF	63	placental growth factor, vascular endothelial growth factor-related protein (PGF)	139326		SEQ ID No : 98	0	SEQ ID No:102	SEQ ID No:103
TNFAIP3	64	tumor necrosis factor, alpha-induced	309943	SEQ ID No : 99		SEQ ID No:388	SEQ ID No:389	SEQ ID No:390

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
		protein 3 (TNFAIP3)						
PHB	65	PHB (prohibitin)	236008	SEQ ID No : 100		SEQ ID No:347	SEQ ID No:348	SEQ ID No:349
RIL	66	LIM domain protein (RIL)	153446		SEQ ID No : 101	0	SEQ ID No:162	SEQ ID No:163
MYBL2	67	v-myb avian myeloblastosis viral oncogene homolog-like 2 (MYBL2)	207378	SEQ ID No : 102	SEQ ID No : 103	SEQ ID No:308	SEQ ID No:309	SEQ ID No:310
RELB	68	v-rel avian reticuloendotheliosis oncogene homolog B (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3) (RELB)	66969	SEQ ID No : 104	SEQ ID No : 105	SEQ ID No:417	SEQ ID No:418	SEQ ID No:419
EST R97218	69	Est R97218	200394	SEQ ID No : 106		SEQ ID No:296	SEQ ID No:297	0
GZMH	70	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1) (GZMB) (ex GZMH)	154343	SEQ ID No : 107		SEQ ID No:178	0	SEQ ID No:179
MYC	71	c-myc proto-oncogene	129438	SEQ ID No : 108	SEQ ID No : 109	SEQ ID No:73	SEQ ID No:74	SEQ ID No:75
CASP1	72	caspase 4, apoptosis-related cysteine protease (CASP4) (ex CASP1)	131502		SEQ ID No : 110	SEQ ID No:84	0	SEQ ID No:85
SYK	73	spleen tyrosine kinase (SYK)	128142	SEQ ID No : 111	SEQ ID No : 112	SEQ ID No:68	SEQ ID No:69	SEQ ID No:70
EST H27202	74	EST H27202 transcription factor E1AF gene	158347	SEQ ID No : 113	SEQ ID No : 114	SEQ ID No:204	SEQ ID No:205	0
HRB	75	syndecan 1 (SDC1) (ex HRB)	108490	SEQ ID No : 115	SEQ ID No : 116	SEQ ID No:1	0	SEQ ID No:2
SHC1	76	p66shc (SHC)	153548		SEQ ID No : 117	0	SEQ ID No:164	SEQ ID No:165
CSF1	77	colony stimulating factor 1 (CSF1)	124554	SEQ ID No : 118	SEQ ID No : 119	SEQ ID No:48	SEQ ID No:49	SEQ ID No:50
UBE3A	78	ubiquitin protein ligase E3A (UBE3A)	141924		SEQ ID No : 120	0	SEQ ID No:104	SEQ ID No:105
FKHR	79	forkhead box O1A (rhabdomyosarcoma) (FOXO1A) (ex FKHR)	151247		SEQ ID No : 121	0	SEQ ID No:133	SEQ ID No:134
CSF1R	80	colony stimulating factor 1 receptor (CSF1R)	196282	SEQ ID No : 122		SEQ ID No:291	0	SEQ ID No:292
IFI75	81	interferon-induced protein 75 (IFI75)	205612	SEQ ID No : 123	SEQ ID No : 124	SEQ ID No:305	SEQ ID No:306	SEQ ID No:307
GATA1	82	GATA-binding protein 1 (globin transcription factor 1) (GATA1)	109093		SEQ ID No : 125	0	SEQ ID No:3	SEQ ID No:4
STAT1	83	signal transducer and activator of transcription 1 (STAT1)	110101		SEQ ID No : 126	0	SEQ ID No:11	SEQ ID No:12
CREBBP	84	CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP)	109677	SEQ ID No : 127	SEQ ID No : 128	SEQ ID No:7	SEQ ID No:8	0
IL7R	85	interleukin 7 receptor (IL7R)	129059		SEQ ID No : 129	0	SEQ ID No:71	SEQ ID No:72
ANXA7	86	annexin A7 (ANXA7)	160580		SEQ ID No : 130	0	SEQ ID No:214	SEQ ID No:215

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
TNXA	87	tenascin XA (TNXA)	124340		SEQ ID No : 131	0	SEQ ID No:46	SEQ ID No:47
CNBP1	88	zinc finger protein 9 (a cellular retroviral nucleic acid binding protein) (ZNF9) (ex CNBP1)	251963	SEQ ID No : 132		SEQ ID No:356	0	SEQ ID No:357
CDK4-a	89	cyclin-dependent kinase 4 (CDK4)	204586	SEQ ID No : 133	SEQ ID No : 134	SEQ ID No:301	SEQ ID No:302	SEQ ID No:288
CSNK2B	90	gene for casein kinase II subunit beta (EC 2.7.1.37)	153879		SEQ ID No : 135	0	SEQ ID No:171	SEQ ID No:172
EFNA1	91	ephrin-A1 (EFNA1)	162997		SEQ ID No : 136	0	SEQ ID No:226	SEQ ID No:227
SELE	92	selectin E (endothelial adhesion molecule 1) (SELE)	186132	SEQ ID No : 137	SEQ ID No : 138	SEQ ID No:259	SEQ ID No:260	SEQ ID No:261
APC	93	adenomatosis polyposis coli (APC)	125284	SEQ ID No : 139	SEQ ID No : 140	SEQ ID No:54	SEQ ID No:55	SEQ ID No:56
FAK	94	PTK2 protein tyrosine kinase 2 (PTK2) (ex FAK)	195731		SEQ ID No : 141	0	SEQ ID No:284	SEQ ID No:285
FOS-a	95	v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS)	208717		SEQ ID No : 142	0	SEQ ID No:317	SEQ ID No:318
FGFR1	96	fibroblast growth factor receptor (FGFR)	154472	SEQ ID No : 143	SEQ ID No : 144	SEQ ID No:180	SEQ ID No:181	SEQ ID No:182
MC1R	97	melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor) (MC1R)	155691		SEQ ID No : 145	0	SEQ ID No:187	SEQ ID No:188
PCNA	98	proliferating cell nuclear antigen (PCNA)	232941	SEQ ID No : 146	SEQ ID No : 147	SEQ ID No:339	SEQ ID No:340	SEQ ID No:341
DDT	99	D-dopachrome tautomerase (DDT)	132109	SEQ ID No : 148	SEQ ID No : 149	SEQ ID No:88	SEQ ID No:89	SEQ ID No:90
GRB2	100	growth factor receptor-bound protein 2 (GRB2)	172152	SEQ ID No : 150	SEQ ID No : 151	SEQ ID No:230	SEQ ID No:231	SEQ ID No:232
AMFR	101	autocrine motility factor receptor (AMFR)	146280	SEQ ID No : 152	SEQ ID No : 153	SEQ ID No:111	SEQ ID No:112	SEQ ID No:113
ITGB2	102	integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit) (ITGB2)	187822	SEQ ID No : 154		0	SEQ ID No:267	SEQ ID No:268
JUND	103	jun D proto-oncogene (JUND)	175421	SEQ ID No : 155		SEQ ID No:233	0	SEQ ID No:234
NF45	104	interleukin enhancer binding factor 2 (ILF2) (ex NF45)	243907		SEQ ID No : 156	0	SEQ ID No:350	SEQ ID No:351
PPP4C	105	protein phosphatase 4 (formerly X) (PPP4C)	114097	SEQ ID No : 157	SEQ ID No : 158	SEQ ID No:32	SEQ ID No:33	SEQ ID No:34
EMS1	106	ATX1 (antioxidant protein 1, yeast) homolog 1 (ATOX1) (ex EMS1)	149172	SEQ ID No : 159		SEQ ID No:123	SEQ ID No:124	SEQ ID No:125
BCL2	107	B-cell CLL/lymphoma 2 (BCL2), nuclear gene encoding mitochondrial protein, transcript variant alpha	147002	SEQ ID No : 160	SEQ ID No : 161	SEQ ID No:115	SEQ ID No:116	SEQ ID No:117
MGST1	108	protein phosphatase 1, catalytic subunit, 182610		SEQ ID No : 162	SEQ ID No : 163	SEQ ID No:248	0	SEQ ID No:249

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
		alpha isoform (PPP1CA) (ex MGST1)						
PDGFRB	109	platelet-derived growth factor receptor, beta polypeptide (PDGFRB)	158976		SEQ ID No : 164	0	SEQ ID No:208	SEQ ID No:209
ANXA11	110	annexin A11 (ANXA11)	158892		SEQ ID No : 165	0	SEQ ID No:206	SEQ ID No:207
GPX1	111	histocompatibility class II antigen gamma chain (CD74) (ex GPX1 Glutathion S transférase)	159809		SEQ ID No : 166	0	SEQ ID No:212	SEQ ID No:213
CFR-1	112	Golgi apparatus protein 1 (GLG1) (ex CFR-1)	153974	SEQ ID No : 167	SEQ ID No : 168	SEQ ID No:173	SEQ ID No:174	SEQ ID No:175
BTF3L3	113	basic transcription factor 3 (BTF3)	195889	SEQ ID No : 169		SEQ ID No:289	0	SEQ ID No:290
EST R55460	114	EST R55460	154997		SEQ ID No : 170	0	SEQ ID No:185	0
AKT2	115	v-akt murine thymoma viral oncogene homolog 2 (AKT2)	183552	SEQ ID No : 171		SEQ ID No:253	0	SEQ ID No:254
CDKN1A	116	cyclin-dependent kinase inhibitor (CDKN1A)	152524	SEQ ID No : 172	SEQ ID No : 173	SEQ ID No:144	SEQ ID No:145	SEQ ID No:146
PPP2CA	117	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform (PPP2CA)	154885	SEQ ID No : 174	SEQ ID No : 175	0	SEQ ID No:183	SEQ ID No:184
MDM2	118	mouse double minute 2, human homolog of, p53-binding protein (MDM2), transcript variant MDM2	148052	SEQ ID No : 176		0	SEQ ID No:120	SEQ ID No:121
TNFRSF6	119	tumor necrosis factor receptor superfamily, member 6 (TNFRSF6)	151767	SEQ ID No : 177	SEQ ID No : 178	SEQ ID No:141	SEQ ID No:142	SEQ ID No:143
CNTFR	120	ciliary neurotrophic factor receptor (CNTFR)	156431		SEQ ID No : 179	0	SEQ ID No:192	SEQ ID No:193
JUNB	121	Jun B proto-oncogene (JUNB)	153213	SEQ ID No : 180	SEQ ID No : 181	SEQ ID No:153	SEQ ID No:154	SEQ ID No:155
CCND1	122	cyclin D1 (PRAD1; parathyroid adenomatosis 1) (CCND1)	110022	SEQ ID No : 182		SEQ ID No:9	0	SEQ ID No:10
TDPX1	123	peroxiredoxin 2 (PRDX2) (ex TDPX1)	208439	SEQ ID No : 183	SEQ ID No : 184	SEQ ID No:314	SEQ ID No:315	SEQ ID No:316
GRB7	124	growth factor receptor-bound protein 7 (GRB7)	130323	SEQ ID No : 185	SEQ ID No : 186	SEQ ID No:79	SEQ ID No:80	SEQ ID No:81
RBBP7	125	retinoblastoma-binding protein 7 (RBBP7)	210874	SEQ ID No : 187	SEQ ID No : 188	SEQ ID No:319	SEQ ID No:320	SEQ ID No:321
TIMP1	126	tissue inhibitor of metalloproteinase 1 (MMP1) (MMP1) (TIMP1)	162246	SEQ ID No : 189	SEQ ID No : 190	SEQ ID No:223	SEQ ID No:224	SEQ ID No:225
YES1	127	y-yes-1 Yamaguchi sarcoma viral oncogene homolog 1 (YES1)	204634	SEQ ID No : 191		SEQ ID No:303	0	SEQ ID No:304
RNF5	128	ring finger protein 5 (RNF5)	112098		SEQ ID No : 192	0	SEQ ID No:25	SEQ ID No:26
PRKCSH	129	protein kinase C substrate 80K-H (PRKCSH)	187232		SEQ ID No : 193	0	SEQ ID No:263	SEQ ID No:264

Symbole gène	N°	Nom	Image	seq3' US PROV LISTING	seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
CTSD	130	cathepsin D (lysosomal aspartyl protease) (CTSD)	149401	SEQ ID No : 194	SEQ ID No : 195	SEQ ID No:126	SEQ ID No:127	SEQ ID No:128
NEO1	131	neogenin (chicken) homolog 1 (NEO1)	188380		SEQ ID No : 196	0	SEQ ID No:269	SEQ ID No:270
GAPD-a	132	glyceraldehyde-3-phosphate dehydrogenase (GAPD)	152847	SEQ ID No : 197		SEQ ID No:150	SEQ ID No:151	SEQ ID No:152
ACTG1	133	actin, gamma 1 (ACTG1)	182291	SEQ ID No : 198	SEQ ID No : 199	SEQ ID No:242	SEQ ID No:243	SEQ ID No:244
ITGA6	134	integrin, alpha 6 (ITGA6)	182431	SEQ ID No : 200	SEQ ID No : 201	SEQ ID No:245	SEQ ID No:246	SEQ ID No:247
GAPD-b	135	glyceraldehyde-3-phosphate dehydrogenase (GAPD)	153607	SEQ ID No : 202	SEQ ID No : 203	SEQ ID No:166	SEQ ID No:167	SEQ ID No:152
ETV5-b	136	ets variant gene 5 (ets-related molecule) (ETV5)	203394	SEQ ID No : 204	SEQ ID No : 205	SEQ ID No:298	SEQ ID No:299	SEQ ID No:300
CDK4-b	137	cyclin-dependent kinase 4 (CDK4)	195800	SEQ ID No : 206	SEQ ID No : 207	SEQ ID No:286	SEQ ID No:287	SEQ ID No:288
FOS-b	138	v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS)	363796	SEQ ID No : 208	SEQ ID No : 209	SEQ ID No:404	SEQ ID No:405	SEQ ID No:318
HOXA5	139	homeobox protein (HOX-1.3) (ex Hox A5)	300564	SEQ ID No : 210	SEQ ID No : 211	SEQ ID No:382	SEQ ID No:383	SEQ ID No:384
RELA	140	NF-kappa-B transcription factor p65 DNA binding subunit (ex RELa)	122056	SEQ ID No : 212		SEQ ID No:42	0	SEQ ID No:43
SUI1	141	S100 calcium-binding protein A11 (caligizarin) (S100A11)	155345	SEQ ID No : 213	SEQ ID No : 214	SEQ ID No:186	0	0
ANG	142	angiotensin, ribonuclease, RNase A family, 5 (ANG)	156720		SEQ ID No : 215	0	SEQ ID No:194	SEQ ID No:195
ITGA6	143	integrin, alpha 6 (ITGA6)	182431	SEQ ID No : 216	SEQ ID No : 217	SEQ ID No:245	SEQ ID No:246	SEQ ID No:247
PRMT2	144	HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 1 (HRMT1L1) (ex PRMT2)	158038	SEQ ID No : 218	SEQ ID No : 219	SEQ ID No:201	SEQ ID No:202	SEQ ID No:203
EST R55460	145	EST R55460	154997		SEQ ID No : 220	0	SEQ ID No:185	0
GZMA	146	granzyme A (granzyme 1, cytotoxic T- lymphocyte-associated serine esterase 3) (GZMA)	356763	SEQ ID No : 221	SEQ ID No : 222	SEQ ID No:402	0	SEQ ID No:403
SOX9	147	SRY (sex-determining region Y)-box 9 (campomelic dysplasia, autosomal sex- reversal) (SOX9)	323948	SEQ ID No : 223		SEQ ID No:394	0	SEQ ID No:395
SRF	148	serum response factor (c-fos serum response element-binding transcription factor) (SRF)	321329		SEQ ID No : 224	SEQ ID No:391	SEQ ID No:392	SEQ ID No:393
EDN1	149	endothelin 1 (EDN1)	153424	SEQ ID No : 225		#N/A	#N/A	#N/A
PTPN6	150	protein tyrosine phosphatase, non-receptor type 6 (PTPN6)	66778	SEQ ID No : 226		#N/A	#N/A	#N/A
TFAP4	151	transcription factor AP-4 (activating	159093	SEQ ID No : 227		0	SEQ ID No:210	SEQ ID No:211

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
		enhancer binding protein 4 (TFAP4)						
ELF1	152	Human cis-acting sequence.Elf-1	182007	SEQ ID No : 228		SEQ ID No:437	0	0
CD2	153	CD2 antigen (p50), sheep red blood cell receptor (CD2)	120649	SEQ ID No : 229		SEQ ID No:431	0	0
CCND2	154	cyclin D2 (CCND2)	175256	SEQ ID No : 230		#N/A	#N/A	#N/A
IL3RA	155	interleukin 3 receptor (hIL-3Ra)	183087	SEQ ID No : 231		SEQ ID No:440	SEQ ID No:441	0
JUP	156	junction plakoglobin (JUP)	157958	SEQ ID No : 232		#N/A	#N/A	#N/A
RBL2	157	retinoblastoma-like 2 (p130) (RBL2)	108571	SEQ ID No : 233		SEQ ID No:430	0	0
HOXA4	158	homeo box A4 (HOXA4)	110731	SEQ ID No : 234		SEQ ID No:20	SEQ ID No:21	0
ACY1	159	aminoacylase 1 (ACY1)	160764	SEQ ID No : 235		SEQ ID No:435	SEQ ID No:436	0
GADD45A	160	growth arrest and DNA-damage-inducible, alpha (GADD45A)	115176	SEQ ID No : 236		#N/A	#N/A	#N/A
nm23	161	non-metastatic cells 1, protein (NM23A) expressed in (NME1)	174388	SEQ ID No : 237		#N/A	#N/A	#N/A
BBC1	162	ribosomal protein L13 (RPL13) (ex BBC1)	178317	SEQ ID No : 238		#N/A	#N/A	#N/A
VEGFB	163	vascular endothelial growth factor B (VEGFB)	162499	SEQ ID No : 239		#N/A	#N/A	#N/A
LAMR1	164	laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1)	199837	SEQ ID No : 240		#N/A	#N/A	#N/A
IL2RB	165	interleukin 2 receptor, beta (IL2RB)	139073	SEQ ID No : 241	SEQ ID No : 242	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
DES	166	desmin	153854	SEQ ID No : 243		SEQ ID No:168	SEQ ID No:169	SEQ ID No:170
PRL	167	prolactin	133738	SEQ ID No : 244		SEQ ID No:91	SEQ ID No:92	SEQ ID No:93
CSH1	168	Chorionic somatomammotropin hormone 1 (placental lactogen) = LACTOGEN Precursor	133891		SEQ ID No : 245	SEQ ID No:432	0	0
TEK	169	tyrosine proteine kinase receptor	151501	SEQ ID No : 246	SEQ ID No : 247	SEQ ID No:138	SEQ ID No:139	SEQ ID No:140
Nrg1	170	neuregulin 1 (EST R72075)	155716	SEQ ID No : 248	SEQ ID No : 249	SEQ ID No:189	SEQ ID No:190	SEQ ID No:191
PLAT	rien	pas d'EST ni mRNA	160149			SEQ ID No:433	SEQ ID No:434	0
EST AW184517	rien		Image ?					

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CLAIMS

1. A polynucleotide library useful in the molecular characterization of a carcinoma, said library comprising a pool of polynucleotide sequences or subsequences thereof wherein said sequences or subsequences are either underexpressed or overpressed in tumor cells, further wherein said sequences or subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID Nos: 1 - 468 or the complement thereof.

2. A polynucleotide library according to Claim 1 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in anyone of the following predefined sets :

SET 1: (SEQ ID No:1; SEQ ID No:2); SET 2: (SEQ ID No:3; SEQ ID No:4); SET 3: (SEQ ID No:5; SEQ ID No:6); SET 4: (SEQ ID No:7; SEQ ID No:8); SET 5: (SEQ ID No:9; SEQ ID No:10); SET 6: (SEQ ID No:11; SEQ ID No:12); SET 7: (SEQ ID No:13; SEQ ID No:14; SEQ ID No:15); SET 8: (SEQ ID No:16); SET 9: (SEQ ID No:17; SEQ ID No:18; SEQ ID No:19); SET 10: (SEQ ID No:20; SEQ ID No:21); SET 11: (SEQ ID No:22; SEQ ID No:23; SEQ ID No:24); SET 12: (SEQ ID No:25; SEQ ID No:26); SET 13: (SEQ ID No:27; SEQ ID No:28; SEQ ID No:29); SET 14: (SEQ ID No:30; SEQ ID No:31); SET 15: (SEQ ID No:32; SEQ ID No:33; SEQ ID No:34) ; SET 16 : (SEQ ID No:35) ; SET 17 : (SEQ ID No:36; SEQ ID No:37; SEQ ID No:38) ; SET 18 : (SEQ ID No:39; SEQ ID No:40; SEQ ID No:41) ; SET 19 : (SEQ ID No:42; SEQ ID No:43) ; SET 20 : (SEQ ID No:44; SEQ ID No:45) ; SET 21 : (SEQ ID No:46; SEQ ID No:47) ; SET 22 : (SEQ ID No:48; SEQ ID No:49; SEQ ID No:50) ; SET 23 : (SEQ ID No:51; SEQ ID No:52; SEQ ID No:53) ; SET 24: (SEQ ID No:54; SEQ ID No:55; SEQ ID No:56) ; SET 25: (SEQ ID No:57; SEQ ID No:58) ; SET 26: (SEQ ID No:59; SEQ ID No:60; SEQ ID No:61) ; SET 27: (SEQ ID No:62; SEQ ID No:63; SEQ ID No:64) ; SET 28: (SEQ ID No:65; SEQ ID No:66; SEQ ID No:67) ;

5 SET 29: (SEQ ID No:68; SEQ ID No:69; SEQ ID No:70) ; SET 30: (SEQ
ID No:71; SEQ ID No:72) ; SET 31 : (SEQ ID No:73; SEQ ID No:74;
SEQ ID No:75) ; SET 32 : (SEQ ID No:76; SEQ ID No:77; SEQ ID
No:78) ; SET 33 : (SEQ ID No:79; SEQ ID No:80; SEQ ID No:81) ; SET
10 34: (SEQ ID No:82; SEQ ID No:83) ; SET 35: (SEQ ID No:84; SEQ ID
No:85) ; SET 36: (SEQ ID No:86; SEQ ID No:87) ; SET 37: (SEQ ID
No:88; SEQ ID No:89; SEQ ID No:90) ; SET 38: (SEQ ID No:91; SEQ ID
No:92; SEQ ID No:93) ; SET 39: (SEQ ID No:94; SEQ ID No:95; SEQ ID
No:96) ; SET 40: (SEQ ID No:97; SEQ ID No:98; SEQ ID No:99) ; SET
15 41: (SEQ ID No:100; SEQ ID No:101; SEQ ID No:78) ; SET 42: (SEQ ID
No:102; SEQ ID No:103) ; SET 43: (SEQ ID No:104; SEQ ID No:105) ;
SET 44: (SEQ ID No:106; SEQ ID No:107; SEQ ID No:108) ; SET 45:
(SEQ ID No:109; SEQ ID No:110) ; SET 46: (SEQ ID No:111; SEQ ID
No:112; SEQ ID No:113) ; SET 47: (SEQ ID No:114) ; SET 48: (SEQ ID
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SEQ ID No:119) ; SET 50: (SEQ ID No:120; SEQ ID No:121) ; SET 51:
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No:124; SEQ ID No:125) ; SET 53: (SEQ ID No:126; SEQ ID No:127;
SEQ ID No:128) ; SET 54: (SEQ ID No:129; SEQ ID No:130) ; SET 55:
25 (SEQ ID No:131; SEQ ID No:132) ; SET 56: (SEQ ID No:133; SEQ ID
No:134) ; SET 57: (SEQ ID No:135; SEQ ID No:136; SEQ ID No:137) ;
SET 58: (SEQ ID No:138; SEQ ID No:139; SEQ ID No:140) ; SET 59:
(SEQ ID No:141; SEQ ID No:142; SEQ ID No:143) ; SET 60: (SEQ ID
No:144; SEQ ID No:145; SEQ ID No:146) ; SET 61: (SEQ ID No:147;
30 SEQ ID No:148; SEQ ID No:149) ; SET 62: (SEQ ID No:150; SEQ ID
No:151; SEQ ID No:152) ; SET 63: (SEQ ID No:153; SEQ ID No:154;
SEQ ID No:155) ; SET 64: (SEQ ID No:156; SEQ ID No:157; SEQ ID
No:158) ; SET 65: (SEQ ID No:159; SEQ ID No:160; SEQ ID No:161) ;
SET 66: (SEQ ID No:162; SEQ ID No:163) ; SET 67: (SEQ ID No:164;
35 SEQ ID No:165) ; SET 68: (SEQ ID No:166; SEQ ID No:167; SEQ ID
No:152) ; SET 69: (SEQ ID No:168; SEQ ID No:169; SEQ ID No:170) ;
SET 70: (SEQ ID No:171; SEQ ID No:172) ; SET 71: (SEQ ID No:173;
SEQ ID No:174; SEQ ID No:175) ; SET 72: (SEQ ID No:176; SEQ ID
No:177) ; SET 73: (SEQ ID No:178; SEQ ID No:179) ; SET 74: (SEQ ID
No:180; SEQ ID No:181; SEQ ID No:182) ; SET 75: (SEQ ID No:183;
SEQ ID No:184) ; SET 76: (SEQ ID No:185) ; SET 77: (SEQ ID No:186)
; SET 78: (SEQ ID No:187; SEQ ID No:188) ; SET 79: (SEQ ID No:189;

SEQ ID No:190; SEQ ID No:191) ; SET 80: (SEQ ID No:192; SEQ ID No:193) ; SET 81: (SEQ ID No:194; SEQ ID No:195) ; SET 82: (SEQ ID No:196; SEQ ID No:197; SEQ ID No:198) ; SET 83: (SEQ ID No:199; SEQ ID No:200) ; SET 84: (SEQ ID No:201; SEQ ID No:202; SEQ ID No:203) ; SET 85: (SEQ ID No:204; SEQ ID No:205) ; SET 86: (SEQ ID No:206; SEQ ID No:207) ; SET 87: (SEQ ID No:208; SEQ ID No:209) ; SET 88: (SEQ ID No:210; SEQ ID No:211) ; SET 89: (SEQ ID No:212; SEQ ID No:213) ; SET 90: (SEQ ID No:214; SEQ ID No:215) ; SET 91: (SEQ ID No:216; SEQ ID No:217) ; SET 92: (SEQ ID No:218; SEQ ID No:219; SEQ ID No:220) ; SET 93: (SEQ ID No:221; SEQ ID No:222) ; SET 94: (SEQ ID No:223; SEQ ID No:224; SEQ ID No:225) ; SET 95: (SEQ ID No:226; SEQ ID No:227) ; SET 96: (SEQ ID No:228; SEQ ID No:229) ; SET 97: (SEQ ID No:230; SEQ ID No:231; SEQ ID No:232) ; SET 98: (SEQ ID No:233; SEQ ID No:234) ; SET 99: (SEQ ID No:235; SEQ ID No:236; SEQ ID No:237) ; SET 100: (SEQ ID No:238; SEQ ID No:239) ; SET 101: (SEQ ID No:240; SEQ ID No:241) ; SET 102: (SEQ ID No:242; SEQ ID No:243; SEQ ID No:244) ; SET 103: (SEQ ID No:245; SEQ ID No:246; SEQ ID No:247) ; SET 104: (SEQ ID No:248; SEQ ID No:249) ; SET 105: (SEQ ID No:250; SEQ ID No:251; SEQ ID No:252) ; SET 106: (SEQ ID No:253; SEQ ID No:254) ; SET 107: (SEQ ID No:255; SEQ ID No:256) ; SET 108: (SEQ ID No:257; SEQ ID No:258) ; SET 109: (SEQ ID No:259; SEQ ID No:260; SEQ ID No:261) ; SET 110: (SEQ ID No:262; SEQ ID No:263; SEQ ID No:264) ; SET 111: (SEQ ID No:265; SEQ ID No:266) ; SET 112: (SEQ ID No:267; SEQ ID No:268) ; SET 113: (SEQ ID No:269; SEQ ID No:270) ; SET 114: (SEQ ID No:271; SEQ ID No:272) ; SET 115: (SEQ ID No:273; SEQ ID No:274) ; SET 116: (SEQ ID No:275; SEQ ID No:276) ; SET 117: (SEQ ID No:277; SEQ ID No:278) ; SET 118: (SEQ ID No:279; SEQ ID No:280; SEQ ID No:281) ; SET 119: (SEQ ID No:282; SEQ ID No:283; SEQ ID No:284) ; SET 120: (SEQ ID No:285; SEQ ID No:286; SEQ ID No:287; SEQ ID No:288) ; SET 121: (SEQ ID No:289; SEQ ID No:290) ; SET 122: (SEQ ID No:291; SEQ ID No:292) ; SET 123: (SEQ ID No:293; SEQ ID No:294; SEQ ID No:295) ; SET 124: (SEQ ID No:296; SEQ ID No:297) ; SET 125: (SEQ ID No:298; SEQ ID No:299; SEQ ID No:300) ; SET 126: (SEQ ID No:301; SEQ ID No:302; SEQ ID No:288) ; SET 127: (SEQ ID No:303; SEQ ID No:304) ; SET 128: (SEQ ID No:305; SEQ ID No:306;

SEQ ID No:307) ; SET 131: (SEQ ID No:308; SEQ ID No:309; SEQ ID No:310) ; SET 132: (SEQ ID No:311; SEQ ID No:312; SEQ ID No:313) ; SET 133: (SEQ ID No:314; SEQ ID No:315; SEQ ID No:316) ; SET 134: (SEQ ID No:317; SEQ ID No:318) ; SET 135: (SEQ ID No:319; SEQ ID No:320; SEQ ID No:321) ; SET 136: (SEQ ID No:322; SEQ ID No:323) ; SET 137: (SEQ ID No:324; SEQ ID No:325) ; SET 138: (SEQ ID No:326; SEQ ID No:327; SEQ ID No:328) ; SET 139: (SEQ ID No:329; SEQ ID No:330) ; SET 140: (SEQ ID No:331; SEQ ID No:332; SEQ ID No:333) ; SET 141: (SEQ ID No:334; SEQ ID No:335; SEQ ID No:336) ; SET 142: (SEQ ID No:337; SEQ ID No:338; SEQ ID No:117) ; SET 143: (SEQ ID No:339; SEQ ID No:340; SEQ ID No:341) ; SET 144: (SEQ ID No:342; SEQ ID No:343; SEQ ID No:344) ; SET 145: (SEQ ID No:345; SEQ ID No:346) ; SET 146: (SEQ ID No:347; SEQ ID No:348; SEQ ID No:349) ; SET 147: (SEQ ID No:350; SEQ ID No:351) ; SET 148: (SEQ ID No:352; SEQ ID No:353) ; SET 149: (SEQ ID No:354; SEQ ID No:355) ; SET 150: (SEQ ID No:356; SEQ ID No:357) ; SET 151: (SEQ ID No:358; SEQ ID No:359; SEQ ID No:360) ; SET 152: (SEQ ID No:361; SEQ ID No:31) ; SET 153: (SEQ ID No:362; SEQ ID No:363; SEQ ID No:364) ; SET 154: (SEQ ID No:365; SEQ ID No:366; SEQ ID No:367) ; SET 155: (SEQ ID No:368; SEQ ID No:369; SEQ ID No:300) ; SET 156: (SEQ ID No:370; SEQ ID No:371) ; SET 157: (SEQ ID No:372; SEQ ID No:373; SEQ ID No:108) ; SET 158: (SEQ ID No:374; SEQ ID No:375; SEQ ID No:376) ; SET 159: (SEQ ID No:377; SEQ ID No:378; SEQ ID No:379) ; SET 160: (SEQ ID No:380; SEQ ID No:381) ; SET 161: (SEQ ID No:382; SEQ ID No:383; SEQ ID No:384) ; SET 162: (SEQ ID No:385; SEQ ID No:386; SEQ ID No:387) ; SET 163: (SEQ ID No:388; SEQ ID No:389; SEQ ID No:390) ; SET 164: (SEQ ID No:391; SEQ ID No:392; SEQ ID No:393) ; SET 165: (SEQ ID No:394; SEQ ID No:395) ; SET 166: (SEQ ID No:396; SEQ ID No:397; SEQ ID No:398) ; SET 167: (SEQ ID No:399; SEQ ID No:400; SEQ ID No:117) ; SET 168: (SEQ ID No:401) ; SET 169: (SEQ ID No:402; SEQ ID No:403) ; SET 170: (SEQ ID No:404; SEQ ID No:405; SEQ ID No:318) ; SET 171: (SEQ ID No:406; SEQ ID No:407; SEQ ID No:408) ; SET 172: (SEQ ID No:409; SEQ ID No:410; SEQ ID No:411) ; SET 173: (SEQ ID No:412; SEQ ID No:413) ; SET 174: (SEQ ID No:414; SEQ ID No:415; SEQ ID No:416) ; SET 175: (SEQ ID No:417; SEQ ID No:418; SEQ ID No:419) ; SET 176: (SEQ ID No:420; SEQ ID No:421; SEQ ID No:422) ; SET 177: (SEQ ID No:423;

SEQ ID No:424; SEQ ID No:425) ; SET 178: (SEQ ID No:426; SEQ ID No:427; SEQ ID No:428) ; SET 179: (SEQ ID No:429; SEQ ID No:408) ; SET 180: (SEQ ID No:430) ; SET 181: (SEQ ID No:431) ; SET 182: (SEQ ID No:432) ; SET 183: (SEQ ID No:433; SEQ ID No:434) ; SET 184: (SEQ ID No:435; SEQ ID No:436) ; SET 185: (SEQ ID No:437) ; SET 186: (SEQ ID No:438; SEQ ID No:439) ; SET 187: (SEQ ID No:440; SEQ ID No:441) ; SET 188: (SEQ ID No:442) ; SET 189: (SEQ ID No:444) ; SET 190: (SEQ ID No:445) ; SET 191 (SEQ ID No:446 ; SEQ ID No:447) ; SET 192: (SEQ ID No:448) ; SET 193: (SEQ ID No:449) ; SET 194: (SEQ ID No:450) ; SET 195: (SEQ ID No:451) ; SET 196: (SEQ ID No:452) ; SET 197: (SEQ ID No:453) ; SET 198: (SEQ ID No:454) ; SET 199: (SEQ ID No:455) ; SET 200: (SEQ ID No:456) ; SET 201: (SEQ ID No:457) ; SET 202: (SEQ ID No:458) ; SET 203: (SEQ ID No:459) ; SET 204: (SEQ ID No:460) ; SET 205: (SEQ ID No:461) ; SET 206: (SEQ ID No:462) ; SET 207: (SEQ ID No:463) ; SET 208: (SEQ ID No:464) ; SET 209: (SEQ ID No:465) ; SET 210: (SEQ ID No:466) ; SET 211: (SEQ ID No:467) ; SET 212: (SEQ ID No:468)

3. A polynucleotide library according to Claim 2 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

4. A library according to anyone Claim 1 or 2 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 1: (SEQ ID No:1 ; SEQ ID No:2) ; SET 4: (SEQ ID No:7 ; SEQ ID No:8) ; SET 18: (SEQ ID No:39 ; SEQ ID No:40 ; SEQ ID No:41) ; SET 21: (SEQ ID No:46 ; SEQ ID No:47) ; SET 24: (SEQ ID No:54 ; SEQ ID No:55 ; SEQ ID No:56) ; SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET 38: (SEQ ID No:91 ; SEQ ID

No:92 ; SEQ ID No:93) ; SET 48: (SEQ ID No:115 ; SEQ ID No:116 ;
SEQ ID No:117) ; SET 53: (SEQ ID No:126 ; SEQ ID No:127 ; SEQ ID
No:128) ; SET 58: (SEQ ID No:138 ; SEQ ID No:139 ; SEQ ID No:140)
; SET 59: (SEQ ID No:141 ; SEQ ID No:142 ; SEQ ID No:143) ; SET
5 61: (SEQ ID No:147 ; SEQ ID No:148 ; SEQ ID No:149) ; SET 64: (SEQ
ID No:156 ; SEQ ID No:157 ; SEQ ID No:158) ; SET 66: (SEQ ID
No:162 ; SEQ ID No:163) ; SET 69: (SEQ ID No:168 ; SEQ ID No:169;
SEQ ID No:170) ; SET 73: (SEQ ID No:178; SEQ ID No:179) ; SET 85:
10 (SEQ ID No:204; SEQ ID No:205) ; SET 88: (SEQ ID No:210; SEQ ID
No:211) ; SET 91: (SEQ ID No:216; SEQ ID No:217) ; SET 97: (SEQ ID
No:230; SEQ ID No:231; SEQ ID No:232) ; SET 104: (SEQ ID No:248;
SEQ ID No:249) ; SET 105: (SEQ ID No:250 ; SEQ ID No:251 ; SEQ ID
No:252) ; SET 112: (SEQ ID No:265 ; SEQ ID No:266) ; SET 113: (SEQ
15 ID No:267 ; SEQ ID No:268) ; SET 115 ; (SEQ ID No:271 ; SEQ ID
No:272) ; SET 131: (SEQ ID No:308 ; SEQ ID No:309 ; SEQ ID No:310)
; SET 132: (SEQ ID No:311 ; SEQ ID No:312 ; SEQ ID No:313) ; SET
134: (SEQ ID No:317 ; SEQ ID No:318) ; SET 137: (SEQ ID No:324 ;
SEQ ID No:325) ; SET 145: (SEQ ID No:345 ; SEQ ID No:346) ; SET
20 147: (SEQ ID No:350 ; SEQ ID No:351) ; SET 155: (SEQ ID No:368 ;
SEQ ID No:369 ; SEQ ID No:300) ; SET 175: (SEQ ID No:417 ; SEQ ID
No:418 ; SEQ ID No:419) ; SET 180: (SEQ ID No:430) ; SET 181: (SEQ
ID No:431) ; SET 182: (SEQ ID No:432) ; SET 185: (SEQ ID No:437) ;
SET 187: (SEQ ID No:440 ; SEQ ID No:441,

wherein said sequences are useful in
25 differentiating a normal cell from a cancer cell.

5. A polynucleotide library according to Claim
4 wherein said polynucleotide sequences or subsequences
thereof of said pool correspond to any combination of at
30 least one polynucleotide selected among those included in at
least 50%, preferably 75% and more preferably 100% of the
predefined sets.

6. A polynucleotide library according to Claim 4
35 wherein the pool of polynucleotide sequences or subsequences

correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

5 SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78)
; SET 73: (SEQ ID No:178 ; SEQ ID No:179) ; SET 131: (SEQ ID
No:308 ; SEQ ID No:309 ; SEQ ID No:310) ; SET 145: (SEQ ID No:345
; SEQ ID No:346) and SET 181: (SEQ ID No:431)

10 and of at least one polynucleotide sequence
selected among those included in each one of predefined
polynucleotide sequences sets comprising:

15 SET 38: (SEQ ID No:91 ; SEQ ID No:92 ; SEQ ID No:93)
; SET 58: (SEQ ID No:138 ; SEQ ID No:139 ; SEQ ID No:140); SET 61:
(SEQ ID No:147 ; SEQ ID No:148 ; SEQ ID No:149); SET 69: (SEQ ID
No:168 ; SEQ ID No:169 ; SEQ ID No:170) and SET 182: (SEQ ID
No:432).

20 7 A polynucleotide library according to Claim
6 wherein said polynucleotide sequences or subsequences
thereof of said pool correspond to any combination of at
least one polynucleotide selected among those included in at
least 50%, preferably 75% and more preferably 100% of the
predefined sets.

25 8. A library according to anyone Claim 1 or 2
wherein the pool of polynucleotide sequences or subsequences
correspond substantially to any combination of at least one
polynucleotide sequence selected among those included in each
one of predefined polynucleotide sequences sets comprising:

30 SET 11: (SEQ ID No:22 ; SEQ ID No:23 ; SEQ ID No:24)
; SET 26: (SEQ ID No:59; SEQ ID No:60 ; SEQ ID No:61) ; SET 32:
(SEQ ID No:76; SEQ ID No:77 ; SEQ ID No:78) ; SET 34: (SEQ ID
No:82 ; SEQ ID No:83) ; SET 40: (SEQ ID No:97 ; SEQ ID No:98 ; SEQ
ID No:99) ; SET 57: (SEQ ID No:135 ; SEQ ID No:136 ;SEQ ID No:137)
; SET 64: (SEQ ID No:156 ; SEQ ID No:157; SEQ ID No:158) ; SET
35 107: (SEQ ID No:255 ; SEQ ID No:256) ; SET 119: (SEQ ID No:279 ;

SEQ ID No:280 ; SEQ ID No:281) ; SET 136: (SEQ ID No:322 ; SEQ ID No:323) ; SET 140: (SEQ ID No:331 ; SEQ ID No:332 ; SEQ ID No:333) ; SET 141: (SEQ ID No:334; SEQ ID No:335 ; SEQ ID No:336) ; SET 145: (SEQ ID No:345; SEQ ID No:346) ; SET 148: (SEQ ID No:352; SEQ ID No:353) ; SET 149: (SEQ ID No:354 ; SEQ ID No:355) ; SET 162: (SEQ ID No:385; SEQ ID No:386; SEQ ID No:387) ; SET 165: (SEQ ID No:394 ; SEQ ID No:395) ; SET 169: (SEQ ID No:402 ; SEQ ID No:403) ; SET 174: (SEQ ID No:414 ; SEQ ID No:415 ; SEQ ID No:416) and SET 188: (SEQ ID No:442),

wherein said sequences are useful in detecting a hormone sensitive tumor cell

9. A polynucleotide library according to Claim 8 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

10. A library according to Claim 8 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET 136: (SEQ ID No:322 ; SEQ ID No:323) ; SET 145: (SEQ ID No:345 ; SEQ ID No:346); SET 149: (SEQ ID No:354 ; SEQ ID No:355) and SET 169: (SEQ ID No:402 ; SEQ ID No:403)

and of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 11: (SEQ ID No:22 ; SEQ ID No:23 ; SEQ ID No:24) ; SET 40: (SEQ ID No:97 ; SEQ ID No:98 ; SEQ ID No:99); SET 57: (SEQ ID No:135 ; SEQ ID No:136 ; SEQ ID No:137); SET 119: (SEQ ID

No:279; SEQ ID No:280 ; SEQ ID No:281) and SET 174: (SEQ ID No:414 ; SEQ ID No:415 ; SEQ ID No:416)

11. A polynucleotide library according to Claim
5 10 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

10 12. A library according to anyone Claim 1 or 2 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each
15 one of predefined polynucleotide sequences sets comprising:

SET 8: (SEQ ID No:16) ; SET 11: (SEQ ID No:22 ; SEQ ID No:23 ; SEQ ID No:24) ; SET 18: (SEQ ID No:39 ; SEQ ID No:40 ; SEQ ID No:41) ; SET 25: (SEQ ID No:57 ; SEQ ID No:58) ; SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET 34: (SEQ ID No:82 ; SEQ ID No:83) ; SET 40: (SEQ ID No:97 ; SEQ ID No:98 ; SEQ ID No:99) ; SET 49: (SEQ ID No:118 ; SEQ ID No:119) ; SET 57: (SEQ ID No:135 ; SEQ ID No:136 ; SEQ ID No:137) ; SET 91: (SEQ ID No:216 ; SEQ ID No:217) ; SET 100: (SEQ ID No:238 ; SEQ ID No:239) ; SET 105: (SEQ ID No:250 ; SEQ ID No:251 ; SEQ ID No:252) ; SET 136: (SEQ ID No:322 ; SEQ ID No:323) ; SET 138: (SEQ ID No:326 ; SEQ ID No:327 ; SEQ ID No:328) ; SET 139: (SEQ ID No:329 ; SEQ ID No:330) ; SET 141: (SEQ ID No:334 ; SEQ ID No:335 ; SEQ ID No:336) ; SET 158: (SEQ ID No:374 ; SEQ ID No:375 ; SEQ ID No:376) ; SET 169: (SEQ ID No:402 ; SEQ ID No:403) ; SET 180: (SEQ ID No:430) and SET 186: (SEQ ID No:438 ; SEQ ID No:439),

30 wherein said sequences are useful in differentiating a tumor with lymph nodes from a tumor without lymph nodes.

13. A polynucleotide library according to Claim 12 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

14. A library according to Claim 12 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising

SET 18: (SEQ ID No:39 ; SEQ ID No:40 ; SEQ ID No:41) ; SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET 57: (SEQ ID No:135 ; SEQ ID No:136; SEQ ID No:137); SET 91: (SEQ ID No:216 ; SEQ ID No:217) and SET 105: (SEQ ID No:250 ; SEQ ID No:251 ; SEQ ID No:252)

and of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 11: (SEQ ID No:22 ; SEQ ID No:23; SEQ ID No:24) ; SET 40: (SEQ ID No:97; SEQ ID No:98 SEQ ID No:99) ; SET 49: (SEQ ID No:118 ; SEQ ID No:119) ; SET 100: (SEQ ID No:238 ; SEQ ID No:239) and SET 141: (SEQ ID No:334; SEQ ID No:335 ; SEQ ID No:336).

15. A polynucleotide library according to Claim 14 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

16. A library according to anyone of Claims 1 or 2 wherein the pool of polynucleotide sequences or

subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

5 SET 11: (SEQ ID No:22 ; SEQ ID No:23 ; SEQ ID No:24)
; SET 22: (SEQ ID No:48 ; SEQ ID No:49 ; SEQ ID No:50) ; SET 23:
(SEQ ID No:51 ; SEQ ID No:52 ; SEQ ID No:53) ; SET 26: (SEQ ID
10 No:59 ; SEQ ID No:60 ; SEQ ID No:61) ; SET 28: (SEQ ID No:65 ; SEQ
ID No:66 ; SEQ ID No:67) ; SET 31: (SEQ ID No:73 ; SEQ ID No:74 ;
SEQ ID No:75) ; SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID
No:78) ; SET 34: (SEQ ID No:82 ; SEQ ID No:83) ; SET 49: (SEQ ID
No:118 ; SEQ ID No:119) ; SET 57: (SEQ ID No:135 ; SEQ ID No:136 ;
SEQ ID No:137) ; SET 64: (SEQ ID No:156 ; SEQ ID No:157 ; SEQ ID
No:158) ; SET 73: (SEQ ID No:178 ; SEQ ID No:179) ; SET 77: (SEQ ID
15 No:186) ; SET 81: (SEQ ID No:194 ; SEQ ID No:195) ; SET 95: (SEQ
ID No:226 ; SEQ ID No:227) ; SET 131: (SEQ ID No:308 ; SEQ ID
No:309 ; SEQ ID No:310) ; SET 138: (SEQ ID No:326 ; SEQ ID No:327
; SEQ ID No:328) ; SET 140: (SEQ ID No:331 ; SEQ ID No:332 ; SEQ
ID No:333) ; SET 149: (SEQ ID No:354 ; SEQ ID No:355) ; SET 162:
20 (SEQ ID No:385 ; SEQ ID No:386 ; SEQ ID No:387) ; SET 164: (SEQ ID
No:391 ; SEQ ID No:392 ; SEQ ID No:393) ; SET 165: (SEQ ID No:394
; SEQ ID No:395) and SET 183: (SEQ ID No:433 ; SEQ ID No:434),

 wherein said sequences are useful in
differentiating antracycline-sensitive tumors from
25 antracycline-insensitive tumors.

17. A polynucleotide library according to Claim
16 wherein said polynucleotide sequences or subsequences
thereof of said pool correspond to any combination of at
30 least one polynucleotide selected among those included in at
least 50%, preferably 75% and more preferably 100% of the
predefined sets.

18. A library according to Claim 16 wherein the
35 pool of polynucleotide sequences or subsequences correspond

substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising

5 SET N° 32: (SEQ ID No:76; SEQ ID No:77; SEQ ID No:78)
; SET N°136: (SEQ ID No:322 ; SEQ ID No:323) ; SET N° 145: (SEQ ID
No:345; SEQ ID No:346) ; SET N° 149: SEQ ID No:354; SEQ ID No:355)
; SET N°169: (SEQ ID No:402 ; SEQ ID No:403)

10 and of at least one polynucleotide sequence
selected among those included in each one of predefined
polynucleotide sequences sets comprising:

15 SET No 11: (SEQ ID No:22; SEQ ID No:23 ; SEQ ID
No:24); SET No 40: (SEQ ID No:97 ; SEQ ID No:98 ; SEQ ID No:99) ;
SET No 57: (SEQ ID No:135 ; SEQ ID No:136 ; SEQ ID No:137) ; SET
No 119: (SEQ ID No:279 ; SEQ ID No:280 ; SEQ ID No:281) ; SET No
174: (SEQ ID No:414 ; SEQ ID No:415; SEQ ID No:416).

20 19. A polynucleotide library according to Claim
18 wherein said polynucleotide sequences or subsequences
thereof of said pool correspond to any combination of at
least one polynucleotide selected among those included in at
least 50%, preferably 75% and more preferably 100% of the
predefined sets.

25 20. A library according to anyone of Claims 1 or
2 wherein the pool of polynucleotide sequences or
subsequences correspond substantially to any combination of
at least one polynucleotide sequence selected among those
included in each one of predefined polynucleotide sequences
sets comprising

30 SET No 14 (SEQ ID No:30; SEQ ID No:31) ; SET No 23
(SEQ ID No:51; SEQ ID No:52; SEQ ID No:53) ; SET No 25 (SEQ ID
No:57; SEQ ID No:58) ; SET No 27 (SEQ ID No:62; SEQ ID No:63; SEQ
ID No:64) ; SET No 28 (SEQ ID No:65; SEQ ID No:66; SEQ ID No:67) ;
SET No 32 (SEQ ID No:76; SEQ ID No:77; SEQ ID No:78) ; SET No 39
35 (SEQ ID No:94; SEQ ID No:95; SEQ ID No:96) ; SET No 41 (SEQ ID

No:100; SEQ ID No:101; SEQ ID No:78) ; SET No 44 (SEQ ID No:106;
SEQ ID No:107; SEQ ID No:108) ; SET No 48 (SEQ ID No:115; SEQ ID
No:116; SEQ ID No:117) ; SET No 51 (SEQ ID No:122; SEQ ID No:78) ;
SET No 64 (SEQ ID No:156; SEQ ID No:157; SEQ ID No:158) ; SET No
5 81 (SEQ ID No:194; SEQ ID No:195) ; SET No 83 (SEQ ID No:199; SEQ
ID No:200) ; SET No 91 (SEQ ID No:216; SEQ ID No:217) ; SET No 96
(SEQ ID No:228; SEQ ID No:229) ; SET No 99 (SEQ ID No:235; SEQ ID
No:236; SEQ ID No:237) ; SET No 108 (SEQ ID No:257; SEQ ID No:258)
; SET No 110 (SEQ ID No:262; SEQ ID No:200) ; SET No 116 (SEQ ID
10 No:273; SEQ ID No:274) ; SET No 117 (SEQ ID No:275; SEQ ID No:276)
; SET No 118 (SEQ ID No:277; SEQ ID No:278) ; SET No 120 (SEQ ID
No:282; SEQ ID No:283; SEQ ID No:276) ; SET No 126 (SEQ ID No:296;
SEQ ID No:297;) ; SET No 142 (SEQ ID No:337; SEQ ID No:338; SEQ ID
No:117) ; SET No 144 (SEQ ID No:342; SEQ ID No:343; SEQ ID No:344)
15 ; SET No 149 (SEQ ID No:354; SEQ ID No:355) ; SET No 152 (SEQ ID
No:361; SEQ ID No:31) ; SET No 153 (SEQ ID No:362; SEQ ID No:363;
SEQ ID No:364) ; SET No 154 (SEQ ID No:365; SEQ ID No:366; SEQ ID
No:367) ; SET No 157 (SEQ ID No:372; SEQ ID No:373; SEQ ID No:108)
; SET No 159 (SEQ ID No:377; SEQ ID No:378; SEQ ID No:379) ; SET
20 No 162 (SEQ ID No:385; SEQ ID No:386; SEQ ID No:387) ; SET No 166
(SEQ ID No:396; SEQ ID No:397; SEQ ID No:398) ; SET No 167 (SEQ ID
No:399; SEQ ID No:400; SEQ ID No:117) ; SET No 168 (SEQ ID No:401)
; SET No 171 (SEQ ID No:406; SEQ ID No:407; SEQ ID No:408) ; SET
No 172 (SEQ ID No:409; SEQ ID No:410; SEQ ID No:411) ; SET No 173
25 (SEQ ID No:412; SEQ ID No:413) ; SET No 176 (SEQ ID No:420; SEQ ID
No:421; SEQ ID No:422) ; SET No 177 (SEQ ID No:423; SEQ ID No:424;
SEQ ID No:425) ; SET No 178 (SEQ ID No:426; SEQ ID No:427; SEQ ID
No:428) ; SET No 179 (SEQ ID No:429; SEQ ID No:408) ; SET No 184
(SEQ ID No:435; SEQ ID No:436) ; SET No 185 (SEQ ID No:437),

30 wherein said sequences are useful in classifying
good and poor prognosis primary breast tumors.

21. A polynucleotide library according to Claim
20 wherein said polynucleotide sequences or subsequences
35 thereof of said pool correspond to any combination of at
least one polynucleotide selected among those included in at

least 50%, preferably 75% and more preferably 100% of the predefined sets.

22. A library according to Claim 20 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising

SET N° 23 (SEQ ID No:51 ; SEQ ID No:52 ; SEQ ID No:53) ; SET N° 25 (SEQ ID No:57 ; SEQ ID No:58) ; SET N° 32 (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET N° 41 (SEQ ID No:100 ; SEQ ID No:101 ; SEQ ID No:78) ; SET N° 48 (SEQ ID No:115 ; SEQ ID No:116 ; SEQ ID No:117) ; SET N° 51 (SEQ ID No:122 ; SEQ ID No:78) ; SET N° 64 (SEQ ID No:156 ; SEQ ID No:157 ; SEQ ID No:158) ; SET N° 81 (SEQ ID No:194 ; SEQ ID No:195) ; SET N° 83 (SEQ ID No:199 ; SEQ ID No:200) ; SET N° 91 (SEQ ID No:216 ; SEQ ID No:217) ; SET N° 99 (SEQ ID No:235 ; SEQ ID No:236 ; SEQ ID No:237) ; SET N° 110 (SEQ ID No:262 ; SEQ ID No:200) ; SET N° 116 (SEQ ID No:273 ; SEQ ID No:274) ; SET N° 142 (SEQ ID No:337 ; SEQ ID No:338 ; SEQ ID No:117) ; SET N° 144 (SEQ ID No:342 ; SEQ ID No:343 ; SEQ ID No:344) ; SET N° 149 (SEQ ID No:354 ; SEQ ID No:355) ; SET N° 162 (SEQ ID No:385 ; SEQ ID No:386 ; SEQ ID No:387) ; SET N° 167 (SEQ ID No:399 ; SEQ ID No:400 ; SEQ ID No:117) ; SET N° 171 (SEQ ID No:406 ; SEQ ID No:407 ; SEQ ID No:408) ; SET N° 172 (SEQ ID No:409 ; SEQ ID No:410 ; SEQ ID No:411) ; SET N° 173 (SEQ ID No:412 ; SEQ ID No:413) ; SET N° 176 (SEQ ID No:420 ; SEQ ID No:421 ; SEQ ID No:422) ; SET N° 177 (SEQ ID No:423 ; SEQ ID No:424 ; SEQ ID No:425) ; SET N° 178 (SEQ ID No:426 ; SEQ ID No:427 ; SEQ ID No:428) ; SET N° 179 (SEQ ID No:429 ; SEQ ID No:408) ; SET N° 184 (SEQ ID No:435 ; SEQ ID No:436) ; SET N° 185 (SEQ ID No:437),

and at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET No 14 (SEQ ID No:30 ; SEQ ID No:31) ; SET No 27 (SEQ ID No:62 ; SEQ ID No:63 ; SEQ ID No:64) ; SET No 28 (SEQ ID

No:65 ; SEQ ID No:66 ; SEQ ID No:67) ; SET No 39 (SEQ ID No:94 ;
SEQ ID No:95 ; SEQ ID No:96) ; SET No 44 (SEQ ID No:106 ; SEQ ID
No:107 ; SEQ ID No:108) ; SET No 96 (SEQ ID No:228 ; SEQ ID
No:229) ; SET No 108 (SEQ ID No:257 ; SEQ ID No:258) ; SET No 117
5 (SEQ ID No:275 ; SEQ ID No:276) ; SET No 118 (SEQ ID No:277 ; SEQ
ID No:278) ; SET No 120 (SEQ ID No:282 ; SEQ ID No:283 ; SEQ ID
No:276) ; SET No 126 (SEQ ID No:296 ; SEQ ID No:297) ; SET No 152
(SEQ ID No:361 ; SEQ ID No:31) ; SET No 153 (SEQ ID No:362 ; SEQ
ID No:363 ; SEQ ID No:364) ; SET No 154 (SEQ ID No:365 ; SEQ ID
10 No:366 ; SEQ ID No:367) ; SET No 157 (SEQ ID No:372 ; SEQ ID
No:373 ; SEQ ID No:108) ; SET No 159 (SEQ ID No:377 ; SEQ ID
No:378 ; SEQ ID No:379) ; SET No 166 (SEQ ID No:396 ; SEQ ID
No:397 ; SEQ ID No:398) ; SET No 168 (SEQ ID No:401),

wherein the combination of overexpression of the
15 genes identified by said first group of cluster sequences
with the underexpression of the genes identified by said
second group of cluster sequences are useful in classifying
good and poor prognosis primary breast tumors.

20 23. A polynucleotide library according to Claim
22 wherein said polynucleotide sequences or subsequences
thereof of said pool correspond to any combination of at
least one polynucleotide selected among those included in at
least 50%, preferably 75% and more preferably 100% of the
25 predefined sets.

24. A polynucleotide library according to anyone
of Claims 1 to 23 wherein said tumor cells are breast tumor
cells.

30 25. A polynucleotide library according to any of
Claims 1 to 23 wherein said polynucleotides are immobilized
on a solid support in order to form a polynucleotide array.

26. A polynucleotide library according to Claim 25 wherein the support is selected from the group comprising a nylon membrane, nitrocellulose membrane, glass slide, glass beads, membranes on glass support or a silicon chip.

5

27. A polynucleotide array useful for prognosis or diagnostic of tumor comprising an immobilized polynucleotide library according to Claims 1 to 3.

10

28. A polynucleotide array useful to differentiate a normal cell from a cancer cell comprising any combination of immobilized polynucleotide sequences sets according to claims 4 to 7.

15

29. A polynucleotide array useful to detect a hormone sensitive tumor cell comprising any combination of immobilized polynucleotide sequences sets according to claims 8 to 11.

20

30. A polynucleotide array useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes comprising any combination of immobilized polynucleotide sequences sets according to claims 12 to 15.

25

31. A polynucleotide array useful to differentiate antracycline-sensitive tumors from antracycline-insensitive tumors comprising any combination of immobilized polynucleotide sequences sets according to claims 16 to 19.

30

32. A polynucleotide array useful to classify good and poor prognosis primary breast tumors comprising any

combination of immobilized polynucleotide sequences sets according to claim 20 to 23.

5 33. A method of detecting differentially expressed polynucleotide sequences which are correlated with a cancer, said method comprising:

a) obtaining a polynucleotide sample from a patient and

10 b) reacting said polynucleotide sample obtained in step (a) with a probe immobilized on a solid support wherein said probe comprises any combination of the polynucleotide sequences of the polynucleotide library of Claims 1 to 23 or any combination of expression products encoded by any of the polynucleotide sequences of the
15 libraries of Claims 1 to 23 and

c) detecting the reaction product of step (b).

20 34. A method for detecting differentially expressed polynucleotide sequences according to Claim 33 wherein said polynucleotide sample is labeled before its reaction step.

25 35. A method for detecting differentially expressed polynucleotide sequences according to Claim 34 wherein the label of the polynucleotide sample is selected from the group consisting of radioactive, colorimetric, enzymatic, molecular amplification, bioluminescent or fluorescent labels.

30 36. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 35 further comprising obtaining a control polynucleotide sample, reacting said control sample with said probe

detecting a control sample reaction product and comparing the amount of said polynucleotide sample reaction product to the amount of said control sample reaction product.

5 37. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 36 wherein the polynucleotide sample is cDNA, RNA or mRNA.

10 38. A method for detecting differentially expressed polynucleotide sequences according to Claim 37 wherein mRNA is isolated from said polynucleotide sample and cDNA is obtained by reverse transcription of said mRNA.

15 39. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 38 wherein said reaction step is performed by hybridising the polynucleotide sample with the probe.

20 40. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 39 wherein said method is used for detecting, diagnosing, staging, monitoring, predicting, preventing or treating conditions associated with cancer.

25 41. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 40 wherein the cancer is breast cancer.

30 42. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 41 wherein the product encoded by any of the polynucleotide sequences or polynucleotide sequences sets is involved in a receptor-ligand reaction on which detection is based.

43. A method for screening an anti-tumor agent comprising the method of Claim 33 wherein said polynucleotide sample is obtained from a patient treated with the anti-tumor agent to be screened.

Figure 1

Figure 1A

Normal Breast

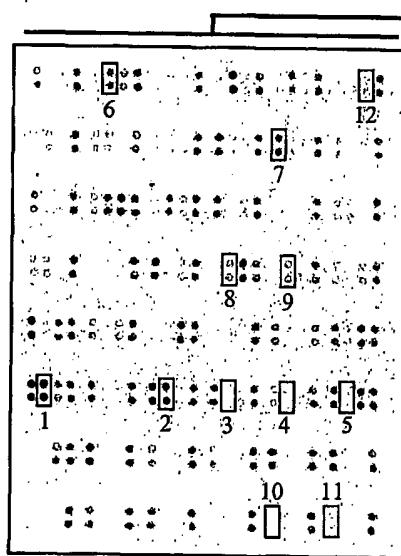
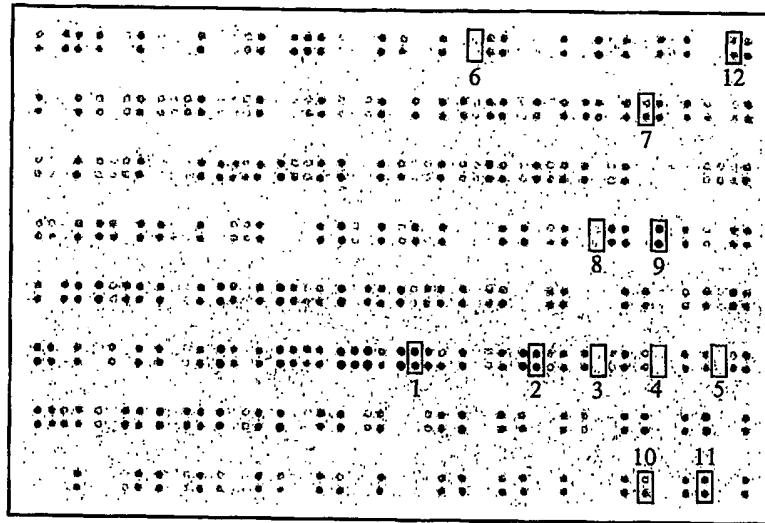
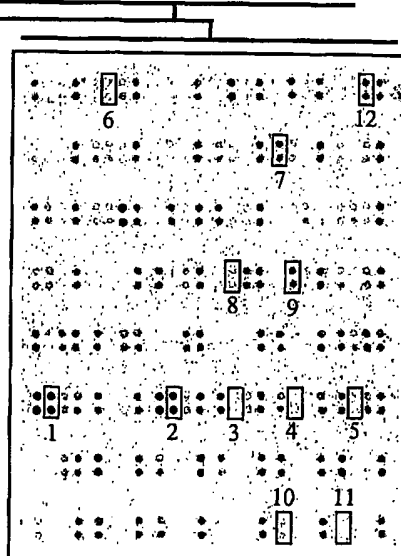


Figure 1B

ER-



ER+

Figure 1C

Breast cancer

Figure 2

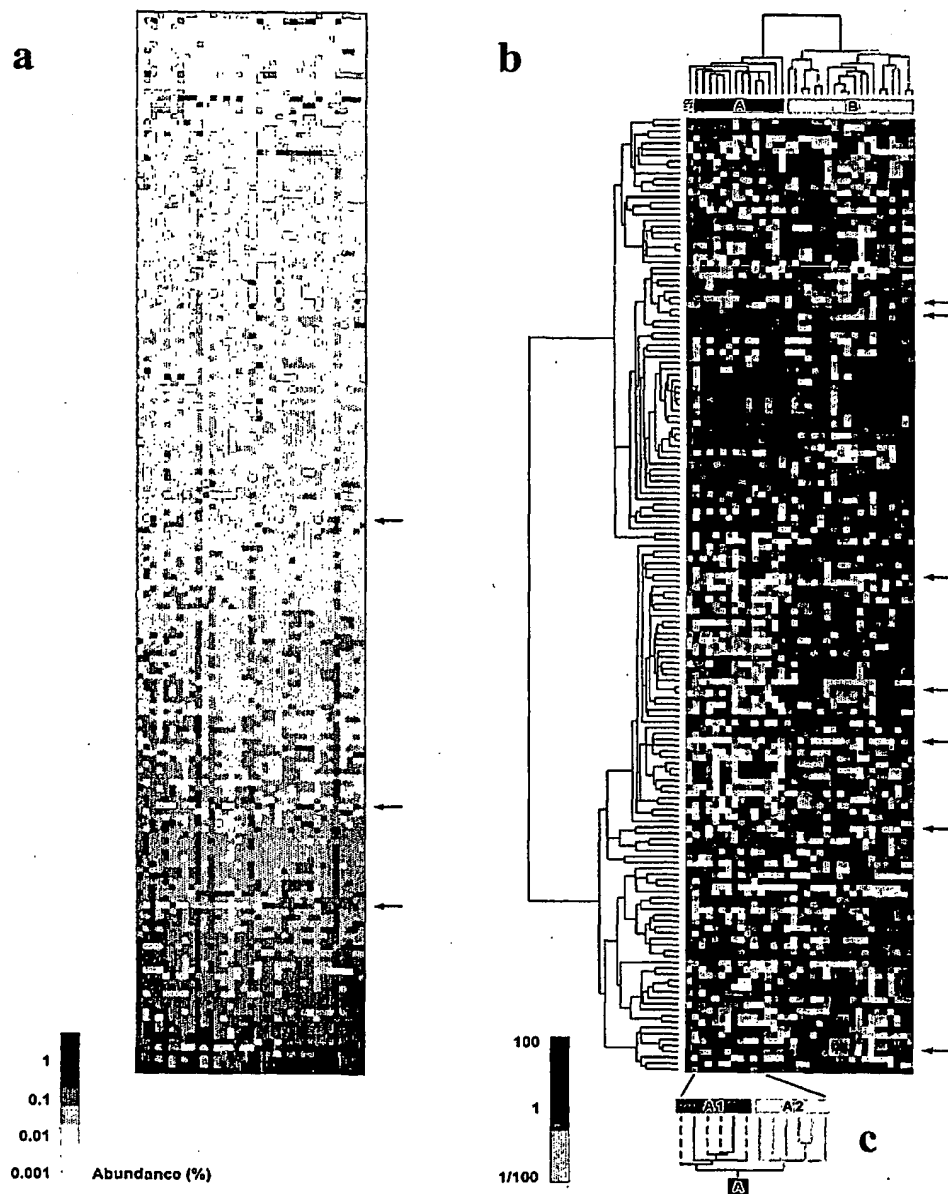


Figure 3

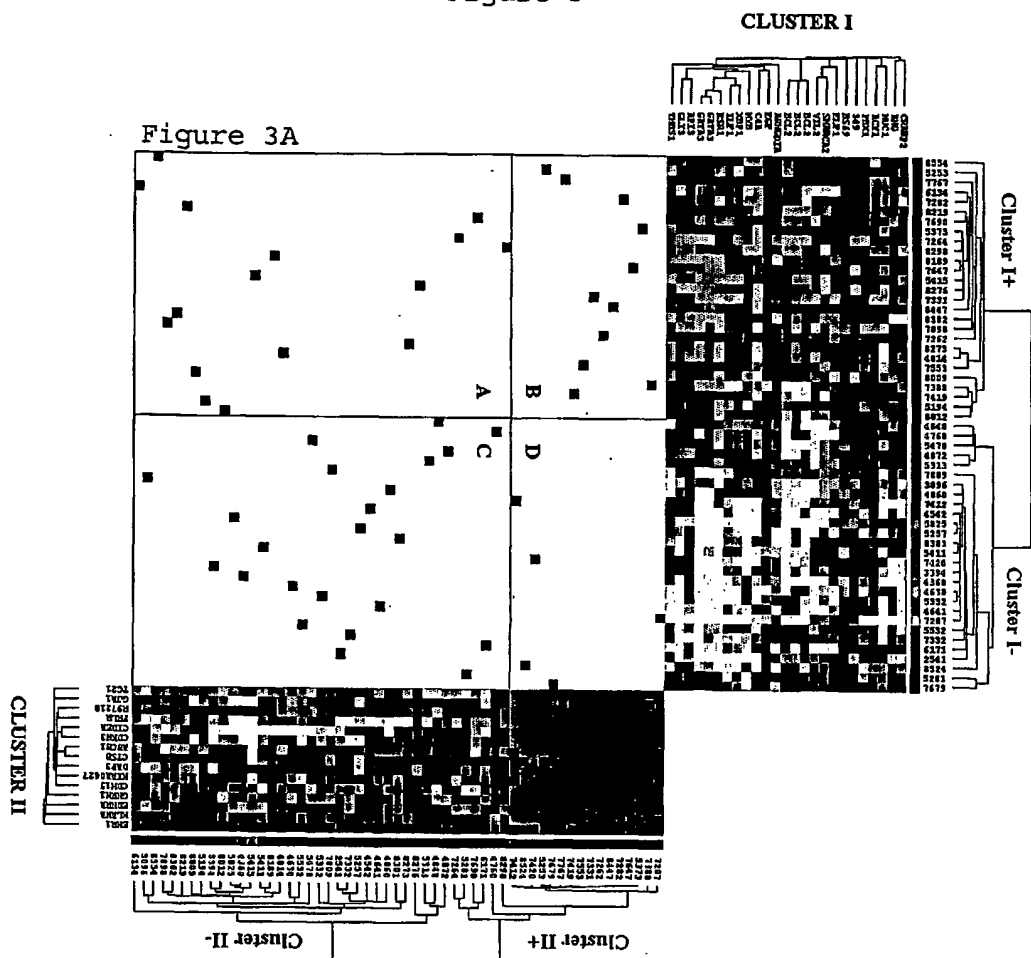


Figure 3C

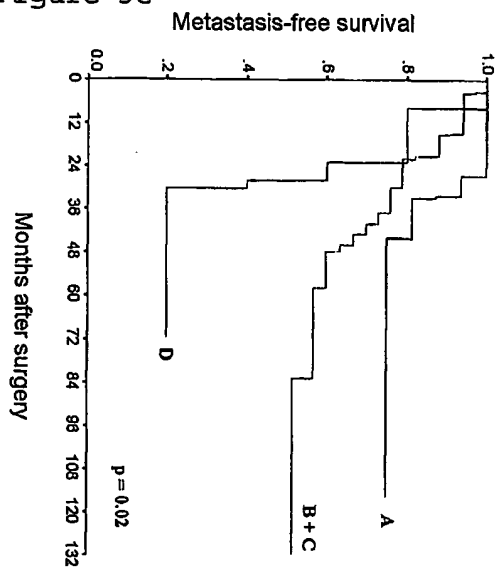


Figure 3B

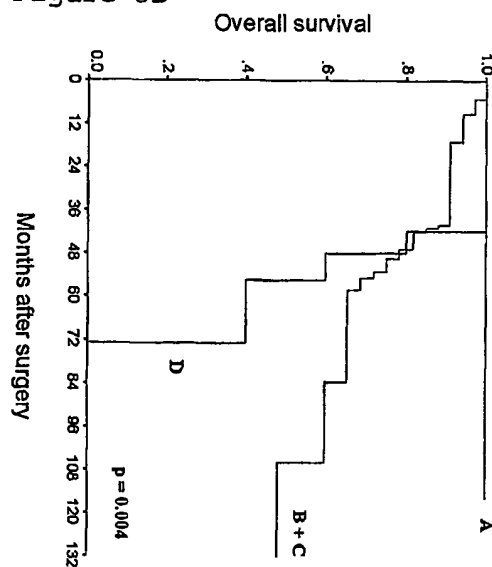


Figure 4

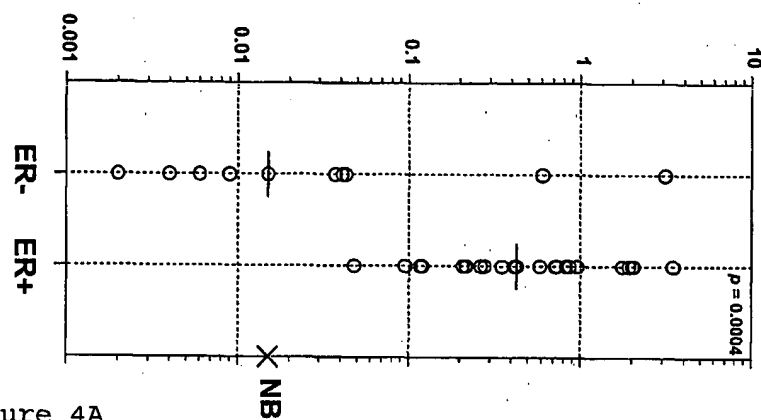


Figure 4A

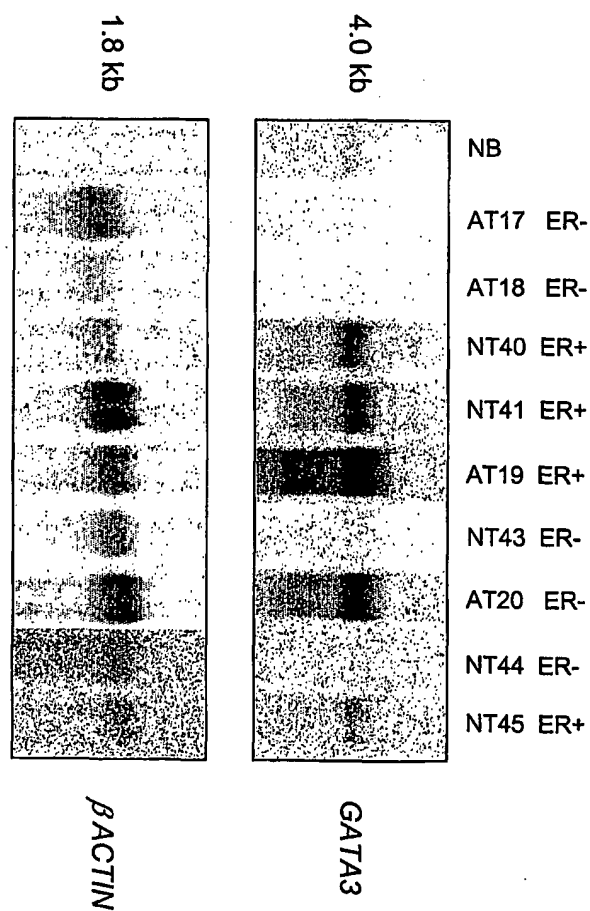


Figure 4B

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<110> François Bertucci
Rémi Houlgatte
Daniel Birnbaum
Catherine Nguyen
Patrice Viens
Fert, vincent

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2/292

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tggcctgtga tccctacttg ttgcctcaca tccgaaagtc agtctctaca agtagccctg 2340
ctggagctgc tattgcatca acctctgggg cgtccaataa cagttcttct aattgagact 2400
gactccaagg ccacaaactg ttcaacacac acaaagtga caaatggcgt tcagcagcgg 2460
gtttggaaca tagcgaatcc gaatggatct gatgaaacct gtaccaggtg cttttatttt 2520
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caaagaatga ggttagaaga ctgcagcttg gagtctct ct aggttttcaa ctatttcttc 3240
acaatttgaa cacttgacgg ttgtcccttt taatttattt gaagtgtat ttttttaa 3300
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```

<210> 7

<211> 300

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(300)

<223> 3' terminal sequence. ests, weakly similar
to alu7_human alu subfamily sq sequence
contamination warning entry [h.sapiens] (EST
T81919) gene.

<400> 7

```

tncaagagac agggtttngc acattgccca ggatggtctc aaactcctag agttgagcta 60
tccaccacc tttggcctnc caaagtgtct ggatcacagg cgtgagtcac tgtntccagc 120
acccatctgg aggtctctta aagcccaggc cccacgccga gcttctgagt caataaagaa 180
gtctgcattt ctaacaagct tctaggggat gctgctgctg ctgctggtcc aggggcccc 240
ctttgaagaa ccactgcact gggnttttcc tctgggaccc gaatgcctgt gcttctcccc 300

```

<210> 8

<211> 369

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<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(369)

<223> 5' terminal sequence. ests, weakly similar
to alu7_human alu subfamily sq sequence
contamination warning entry [h.sapiens] (EST
T81919) gene.

<400> 8

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aggcatggca agggtaagtg aa ctgaagca ctttcaatac ttcctaccta accgcggggt 120
ttccctccga gtaatgcgta aaatgggacc acgtggccca ctctgtttt tctctttggg 180
ctctccacgt gccactcatg cttggaagag acagatttct ttctaggata aagatctctg 240
ccccatttct gtctttttaa atggagaatt ctttaaagaa gtagggacag cttncagggt 300
cagggcagtt tgggaaagtn acaggggcct aattgtgttc cgtggaaacn ggggtaggag 360
gtttgcttt                                     369
```

<210> 9

<211> 255

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(255)

<223> 3' terminal sequence. cyclin d1 (prad1:
parathyroid adenomatosis 1) (CCND1) gene.

<400> 9

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gcaaaggaaa aaacaaccaa caacaaggag aatgaagctt tcccttctgg tatcaaaatg 120
ctccggagag gagggactnt cagtggagca cctggggccg gctccgcctc gctgcgggtg 180
gcggtggcgc ccctngcctg gcgccttcag atgtccacgt cccgcacgtc ggtgggtntg 240
caagccaggt ccacc                                     255
```

<210> 10

<211> 1325

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1325)

<223> cyclin d1 (prad1: parathyroid adenomatosis
1) (CCND1) gene.

<400> 10

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gcgcggggca gcagaagcga gagccgagcg cggaccacag caggaccac agccctcccc 120
agctgcccag gaagagcccc agccatggaa caccagctcc tgtgctgcga agtggaacc 180
atccgccgcg cgtaccccga tgccaacctc ctcaacgacc ggtgctgcg gccatgctg 240
aaggcggagg agacctgcgc gccctcgggtg tctacttca aatgtgtgca gaaggaggtc 300
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tgcgaggagg aggtcttccc gctggccatg aactacctgg accgcttcc tgcgctggag 420
cccgtgaaaa agagccgcct gcagctgctg ggggccactt gcatgttcgt ggctctaaag 480
atgaaggaga ccatccccct gacggccgag aagctgtgca tctacaccga cggtccatc 540
cggcccagg agctgctgca aatggagctg ctctggtga acaagctcaa gtggaacctg 600
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gagaacaaac agatcatccg caaacacg cg cagaccttcg ttgcctcttg tgccacagat 720
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aaagcttcat tctcctgtt gttggtgtt ttttctttg ctctttccc ottccatctc 1200
tgacttaagc aaaagaaaaa gattacccaa aaactgtctt taaaagagag agagagaaaa 1260
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1320
aaaaa 1325

<210> 11
<211> 449
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(449)
<223> 5' terminal sequence. signal transducer and
activator of transcription 1, 91kd (STAT1) gene.

<400> 11
atttgaagt caaagtotta tttgataaag atgtgaatga gagaaatata gtaaaaggat 60
ttaggaagtt caacattttg ggcacgcaca caaaagtgat gaacatggag gagtccacca 120
atggcagttt ggcggtgaa tttcggcacc tgcaattgaa agaacaga aa aatgctggca 180
ccagaacgaa tgagggtcct ctcatcgta ctgaagagct tcaactccctt agttttgaaa 240
cccaattgtg ccagcctggg tttggttaatt gacctcgaga cgacctctct gcccggtgtg 300
ggtgatctcc aacgtcagcc agctcccgag cggttggggc ctccattcct ttgggtacaa 360
catgctgggt ngcggggaac cgggg antc tgttccttnt ttcttgact caaccatgtg 420
ncacggtggg gtttcagntt ttcagaagt 449

<210> 12
<211> 4003
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(4003)

<223> signal transducer and activator of
transcription 1, 91kd (STAT1) gene.

<400> 12

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gccatcctcg agagctgtct aggttaacgt tcgcactctg tgtatataac ctcgacagtc 120
ttggcaccta acgtgctgtg cgtagctgct cctttgggtg aatccccagg cctttgttgg 180
ggcacaaagt ggcaagatgt ctgagtggtg cgaacttcag cagcttgact caaaattcct 240
ggagcagggt caccagcttt atgatgacag ttttcccatg gaaatcagac agtacctggc 300
acagtgggtt gaaaagcaag actgggagca cgctgccaat gatgttt cat ttgccaccat 360
ccgttttcat gacctcctgt cacagctgga tgatcaatat agtcgctttt ctttgagaa 420
taacttcttg ctacagcata acataaggaa aagcaagcgt aatcttcagg ataattttca 480
ggaagaccac atccagatgt ctatgatcat ttacagctgt ctgaaggaa aaaggaaaa 540
tctgaaaaac gccagagat ttaat caggc tcagtcgggg aatattcaga gcacagtgt 600
gttagacaaa cagaagagc ttgacagtaa agtcagaaat gtgaaggaca aggttatgtg 660
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caaaataata gagtgtctga atgtcactga acttaccagg aatgccctga ttaatgatga 900
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gcagcttaaa aagtgtggag aattggaaca gaaatacacc tacgaacatg accctatcac 1080
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gtagataaac tcagaaattt aattcatgtt tcttaaatgg gctactttgt cctttttgtt 3360
attagggttg tatttagtct att agccaca aaattgggaa aggagtagaa aaagcagtaa 3420
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```

ctgacaactt gaataatata ccagagataa tatgagaatc agatcatttc aaaactcatt 3480
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gcgaatgggt ccattctctc tctgtacttt tttccagaca cttttttgag tggatgatgt 36 00
ttcgtgaagt atactgtatt tttacctttt tcttctctta tctactgacac aaaaagtaga 3660
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tctcagtttt tatatagatg gcgagaacct aagtttcagt tgattttaca attgaaatga 3960
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```

<210> 13

<211> 167

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(167)

<223> 3' terminal sequence. fibroblast growth factor receptor 2 (bacteria -expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome) (FGFR2) gene.

<400> 13

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ccacctctgc tcggtgaaaa ttaagaaatt atgtgtaaga acagcattta gcaaatagct 60
attaaaaaaa gagagaccaa tttcttag gt gcattgggac atccatttaa antcaatata 120
aaaaataact ccttgtaaat ntataatata ttattttatac ntaattt 167

```

<210> 14

<211> 414

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(414)

<223> 5' terminal sequence. fibroblast growth factor receptor 2 (bacteria -expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome) (FGFR2) gene.

<400> 14

```

ggacacagaa tggataagcc agccaactgc accaacgaac tgtacatgat gatgaggagc 60
tgttggtcatg cagtgcctcc cagagaccaa cgttcaagca gttggtagaa gacttggatc 120
gaattctcac tctcacaacc aatgaggaat acttggacct cagccaacct ctggaacagt 180
attcacctag ttaccttgac ac aagaagtt cttgttcttc aggagatgat tctgtttttt 240
ctccagaccc catgccttac gaacatgcc ttcctcagta tccacacata aacgggcagt 300
gttttaaaac atgaatgact gtgtctggcc tgncccaa acagggacag gactggggg 360
aacctaggct acattnaggc aggggaggac ccttgccttc ccaggngttt gttt 414

```

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<210> 15
<211> 4667
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(4667)
<223> fibroblast growth factor receptor 2
(bacteria-expressed kinase, keratinocyte growth h
factor receptor, craniofacial dysostosis 1,
crouzon syndrome, pfeiffer syndrome, jackson -weiss
syndrome) (FGFR2) gene.

<400> 15
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gcgtacctgg ccgcgcgcgc cgactgctct c cgggctggc gggggccggc cgcgagcccc 120
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gctggggctg tttcatctgc ctggctcgtg tcaacctggc aaccttgctc ctggcccggc 660
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cccactcact ttgcaatagc cgtgcaagat gaatgcagat tacactgatc ttatgtgtta 4560
caaaattgga gaaagtattt aataaaacct gttaattttt atactgacaa taaaaatgtt 4620
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<210> 16

<211> 483

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(483)

<223> 3' terminal sequence. ests (EST T89980)
gene.

<400> 16

```

gtgttgagct cccaaaaggc ttaaaacttg ctttgtgaat gaatgatott aaatcactag 60
tgaagatgat catggggcat ttgcacatta aagaactaaa atgaaatgaa aaagccatga 120
ctcctcactt aatgctatta aaaaaaatc tgatttggtt aattaacccc acttctcata 180
gtttaattgg gtaatcaacg ttcttgggaa ttc aggttct catgggcacc ctaatagtgt 240
ttagggcccg ggtctctgag gctgctgggg gtgatcccga ggaacaagaa gctgccctat 300
taaaagtaat ctacttgagt tttcccgag tctttgggag ttgttcccta ctgtggggct 360
acttataggg gtagggcccc ccaaatccct cacacttagg tcggccctgc tggttggctg 420
tggggctctg aaangcagcc gctaggangt cccaagcct naacttacc attttctggc 480

```

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ctg

483

<210> 17
<211> 400
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(400)
<223> 3' terminal sequence. protein phosphatase 3
(formerly 2b), catalytic subunit, gamma isoform
(calcineurin a gamma) (PPP3CC) gene.

<400> 17
ntttatatat attgaacata aattaaaaga atttataaaa cagccacctt ttacagaat 60
aatgcagac tgaattataa atgcacctcc acgttgaagt tgttttgagt tgcttttcat 120
tttccaataa taaataaata gaatttggtt ttgagtttta gatccacctg agccacggca 180
ggactctaag tcatgaatgg gctttcttcc cttggtcgct cctgtgcgca gatgntgagt 240
gtgctgaggt tacagatttc attggccac cagcgtgtat gc taccctt cgggggtggg 300
cattcgctca ttaattcggg ccagncct cgcgctttct ttcaaaactc cgggatcttg 360
tgcntggagg cgaggnaccc ctctgatggg cttcccgggg 400

<210> 18
<211> 490
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(490)
<223> 5' terminal sequence. protein phosphatase 3
(formerly 2b), catalytic subunit, gamma isoform
(calcineurin a gamma) (PPP3CC) gene.

<400> 18
cttgagcac tataccaca aactgtccg aggggtgctt tatttctaca gttaccctgc 60
agtttgtgaa tttttgcaga acaataattt actatcaatt atcagagccc atgaagccca 120
agatgctggg tatcgaatgt acaggaagag ccaagccaca ggttttccat cacttattac 180
aattttctct gccccaatt acctagatgt ctataacaat aaagctgctg tgttgaaata 240
tgaaaacaat gtcataaata tcaggcagtt taactgttct ccacaccct actgggcttc 300
caaactttat gggatgttt cacatgggtc ttgaccttt gttgggggga ccccgacac 360
agaggatggc tgggtaaatg tggntcaaca ttatgntct ggatggacgg aactgatttt 420
ctggatggat ggaagcngga tgggaaggca cttacngttt cgtaaggng g ttcttcggg 480
gnttaggttc 490

<210> 19
<211> 2134
<212> DNA/RNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2134)

<223> protein phosphatase 3 (formerly 2b),
catalytic subunit, gamma isoform (calcineurin a
gamma) (PPP3CC) gene.

<400> 19

```
gggccaccct tagcagcggg cgcggtcggg gccgaagcgg tgttccccgc cttagccgct 60
gcgcctccca agagagcggc cggtggggccc tcgtcctgtc agtggcgtcg gaggc cggcc 120
tgcggtggcc gcgcccttct ggtgctcgga caccgctgag gagccggggc cgggcacggc 180
tggtcgacgg ctccggggcag ctaaggctgc ccgaggagaa ggcgcgggcc gcggcgtagg 240
cgcacgtccg gcggggtcct ggagcctgga ggaggccgag gggaccatgt ccgggaggcg 300
cttcacctc tccaccaccg accgcgtcat caa agctgtc ccttttcctc caacccaacg 360
gcttactttc aaggaagtat ttgagaatgg gaaacctaaa gttgatgttt taaaaaacca 420
tttggtaaag gaaggacgac tggaagagga agtagcctta aagataatca atgatggggc 480
tgccatcctg aggcaagaga agactatgat agaagtagat gctccaatca cagtatgtgg 540
tgatattcat ggacaattct ttgacctaat gaagttattt gaagttggag gatcacctag 600
taacacacgc tactcttttc tgggtgacta tgtggacaga ggctatttca gtatagagtg 660
tgtgtgtat ttatggagtt taaagattaa tcatcccaa acattgtttc tgcttcgggg 720
aaatcatgaa tgcaggcatc ttacagacta ttccaccttc aaacaggaat gtc gaatcaa 780
atattcgaa caggtgtatg atgcctgtat ggagacattt gactgtcttc ctcttgctgc 840
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actccctctg ggcgtcctct caggaggcaa gcagactatc gagacagcca tcagagggtt 1620
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gcgaatgcc ccccgaaagg atagcatata cctgtgtggg ccaatgaaat ctgtaacctc 1740
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agtctgccc tgctcaggtg gatctaaaac tcaagaacaa attctattta ttattatt g 1860
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atattattctg taaaaagggtg actgttttat aaattctttt aatttatgtt caatatatat 1980
aaaaagtgca tctgttttgt tttcccttt tttctocata attttaagaa atgaatctga 2040
ttgttgtcaa cacatttgtg aagtcttgtg cta taaaggg gaacttcccc taataaaagg 2100
gccttggaaa cctcaaacct gggtttctga cccc 2134
```

<210> 20

<211> 248

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(248)

<223> 3' terminal sequence. ests (EST T90726)
gene.

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<400> 20
atccatttat tatatccaat gctaaacact accacttgga ctctaagata tgtttatgcc 60
tctctgttta ttctagtttt ttaaaaatca aatatacaag atctacaatt atttatatcc 120
aagatgtcta caccactgcc taagaagcta ttaaaatat t tgtatttggt caatgggnacc 180
cattattcac atgggcctag gattaaaaag tcaatttata ttnggaataa atttntccaa 240
aaaaacca 248

<210> 21
<211> 427
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(427)
<223> 5' terminal sequence. ests (EST T90726)
gene.

<400> 21
taagatacga acgagaaacc tgatttattg ctcatccttc ccttgccctcc ctaatggcaa 60
gcaaaaactct gaacatctga aaaggatgta gttctggaca aatcct gact acccagagga 120
aactcactgt gagattgctg ttgatttgaa ggggtgcttc actaagggtta tattttaaag 180
tagaataaca catgctgagt gtaaaactggg ctttggtattg gtcagctgca gtagtacaaa 240
aacagcatag aatttgagga aaactaaaac tgctatgaga taggctatga ggaaaaactta 300
aaactggcta tgtggttagga aatg atgtta aanttatgtg gggaaagttt ttcccctccn 360
tattacttca cattacaggc ctttngaggg gcntctgggc tctgnaccn gtttgatggg 420
cctttga 427

<210> 22
<211> 294
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(294)
<223> 3' terminal sequence. sry (sex determining
region y)-box 4 (SOX4) gene.

<400> 22
tttcttggtt ttcttttttt ttttccgaaa ccaactgccc tccactgact gccctgtac 60
cacatcaaac agtctcctct cctccacgcc tccgggtctt gggaagtctc acctcactga 120
tttcacgtag aaaagaaggc ggaggccagc agccgcgcgc ncaagctccc caacgtgcaa 180
atccatttca gtttgaccgt gaacccctt ccagttcgtg tctcctccg ccccgcccc 240
tagtccccgc tgctggnctt caacggggtt ntcgggtcat ttcctagcgc cggg 294

<210> 23
<211> 362
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(362)

<223> 5' terminal sequence. sry (sex determining region y)-box 4 (SOX4) gene.

<400> 23

```
ttccggactt gtctgcaccc ccagcaagaa ggcgagttag ttttctagag acttgaagga 60
gtctccccct tcctgcatca ccaccttggg tttgttttat tttgcttctt ggtcaagaaa 120
ggaggggaga acccagcgca cccctcccc ctttttttaa acgcgatgat aagacagaag 180
gctccggggt gacgaatttg gccgatggag nat gttttgg gggaacgccg ggactgagag 240
actccaacggc agggcggaatt cccgtttggg gctttttttt tcctccctct ttttccccct 300
gcccttttg canccggngg agggagntgt tnaaggggag ggagggccag ccagtgttga 360
cc
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362

<210> 24

<211> 2797

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2797)

<223> sry (sex determining region y) -box 4 (SOX4) gene.

<400> 24

```
ttccccagca ttcgagaaac tcctctctac ttagcacgg tctccagact cagccgagag 60
acagcaaaact gcagcgcggt gagagagcga gagagaggga gagagagact ctccagcctg 120
ggaactataa ctctctgctg agaggcgag aactccttc ccaaattctt tggggacttt 180
tctctcttta cccacctccg cccctgctg gagttgagg gccagttcgg ccgccgcgcg 240
cgtcttcccc ttccggcgtgt gcttggcccc gggaaccggg agggcccgcc gatcgcgcgcg 300
cggccgcgcg gagggtgtga' gcgcgcgtgg gcgcccgcc agccgaggcc atggtgcagc 360
aaaccaacaa tgcgagaaac acggaagcgc tgctggccgg cgagagctcg gactcgggcg 420
ccggcctcga gctgggaatc gcctcctccc ccacgccgg ctccaccgcc t ccacgggcg 480
gcaaggccga cgaccgcagc tgggtcaaga ccccgagtgg gcacatcaag cgaccatga 540
acgccttcat ggtgtggtcg cagatcgagc ggcgcaagat catggagcag tcgcccgaca 600
tgcaaacgc cgagatctcc aagcggtgg gcaaacgctg gaagctgctc aaagacagcg 660
acaagatccc ttctattcga gaggcggagc ggctgcccct caagcacatg gctgactacc 720
ccgactacaa gtaccggccc aggaagaagg tgaagtccgg caacgccaac tccagctcct 780
cggccgcgcg ctctccaag ccgggggaga agggagacaa ggtcgggtggc agtggcgggg 840
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cgagtggcgg cggcgccaac tccaaaccgg cgcagaaaaa gagctgcggc tccaaagtgg 960
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tgcgcgccgc ctgcgccgc ccgtccagcg cgcctcgca cgcgtcctc tcggcctcgt 1500
ccactcctc ctcttctcct tcctcggtgt cctcgtcctc cgacgacgag ttcgaagacg 1 560
acctgctcga cctgaacccc agctcaaaact ttgagagcat gtccctgggc agcttcagtt 1620
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cgctcgtcggc gctcgaccgg gacctggatt ttaacttcga gcccggtcc ggctcgact 1680
tcgagttccc ggactactgc acgcccagg tgagcgagat gatctcgga gactggctcg 1740
agtccagcat ctccaacctg gttttcacct actgaa gggc gcgcaggcag ggagaagggc 1800
cgggggggggt aggagaggag aaaaaaaaag tgaaaaaaag aaacgaaaag gacagacgaa 1860
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tctcgtcgtc ggatcaagga gcgcggcggc gttttggacc cgcgtccca tccccacct 1980
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ttcgagtttg ctcccccttg cttgaagaga cccctcccc cttccaacga gcttcggac 2160
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ggcgagtgtt ttcgaaaaa aaaaaagaaa aaaaggg 2797

```

<210> 25

<211> 352

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(352)

<223> 5' terminal sequence. ring finger protein 5
(RNF5) gene.

<400> 25

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acggggggccc caacnanant cgcgagcngg gcgtggcggg cgcgaccttc gaatgt anta 60
tatgttttga gactgctcgg gaagctgtgg tcagtgtgtg tggccacctg tactgttggc 120
catgtcttca tcagtggctg gagacacggc cagaacggca agagtgtcca gtatgtaaag 180
ctgggatcag cacagagaag gttgtcccg tttatggcg agggagccag aagccccagg 240
atcccagatt aaaaactcca ccccgcccc aggc agaga ccagctccg agagcagagg 300
gggattccag ccatttggtg ataccggggg cttccacttn ttcatttggg gt 352

```

<210> 26

<211> 543

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(543)

<223> ring finger protein 5 (RNF5) gene.

<400> 26

```

atggcagcag cggaggagga ggacgggggc cccaagggc caaatcgca gcggggcggg 60
gcgggcgcga ctttgaatg taatatatgt ttggagactg ctcgggaagc tgtgtcagt 120

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gtgtgtggcc acctgtactg ttggccatgt cttcatcagt ggctggagac acggc cagaa 180
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ggcgagggga gccagaagcc ccaggatccc agattaaaaa ctccaccccg ccccagggc 300
cagagaccag ctccggagag cagaggggga ttccagccat ttggtgatac cgggggcttc 360
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catgagcctt tccgccgggg tacaggtgtg gatctgggac agggtcaccc agcctccagc 480
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tga 543

<210> 27

<211> 397

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(397)

<223> 3' terminal sequence. axl receptor tyrosine
kinase (AXL) gene.

<400> 27

gccgtggggt gggaaagtgg gaag gtggag ttttccccag tggcagtgt tagcttggat 60
cctgagaggg agtaccaggt ggagggttgt ctcaggcacc atcctcctgc cctgggctgc 120
tggggagccc ctatcagcag gctgagcggg gctaggggtt ttggaagggc agaggacata 180
gcntccagca ggatggacct cagccgcagt naggcagcta caggaatcct tagggtctgg 240
ctgggttggg gggtcagetc ctctgcagc tccaggggnt tcaggataac ctccaccctc 300
atccatnttn acatagagga tttcgtcagg ctctgggggc aggangcaan gcctttcagt 360
ntgttctcca aatcttccn caactctnta aaacttt 397

<210> 28

<211> 418

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(418)

<223> 5' terminal sequence. axl receptor tyrosine
kinase (AXL) gene.

<400> 28

ctgaatgaga acatgtccgt gtgtgtggcg gacttcgggc tctccaagaa gatctaca at 60
ggggactact accgccagga ccgtatcgcc aagatgccag tcaagtggat tgccattgag 120
agtctagctg accgtgteta caccagcaag agcgatgtgt ggtccttcgg ggtgacaatg 180
tgggagattg ccacaagagg ccaaacccca tatccggggc gtggagaaca gcgagattta 240
tgantatctg cgccagggaa atcgccctgaa gcagcct ncg gactgtcttg gatgggantg 300
ttatgccttg atgttcggcg tncctgggga gcttaaattc ccaggggnc ccgnccaatt 360
ttttacaaag cttncgggga agattttttg gagnacacac ttttaagggc tttncctt 418

<210> 29

<211> 5015

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5015)

<223> axl receptor tyrosine kinase (AXL) gene.

<400> 29

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ccagatagag agacacggcc tcaactggctc agcaccaggg tccccctccc cctcctcagc 120
tccctcctctg gcccctttaa gaaagagctg atcctctcct ctcttgagtt aaccctgat 180
tgtccaggtg gcccttggtc ctggcctggt gggcggaggc aaagggggag ccaggggagg 240
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gctgggcaga gccggtggca agggcctc cc ctgccgctgt gccaggcagg cagtgcacaa 360
tccggggagc ctggagctgg ggggagggcc ggggacagcc cgcccgcctg cccctcccc 420
cgctgggagc ccagcaactt ctgaggaaag ttggcacc cc atggcgctggc ggtgccccag 480
gatgggcagg gtcccgcctg cctggtgctt ggcgctgtgc ggctgggctg gcatggcccc 540
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```

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```

<210> 30

<211> 439

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(439)

<223> 5' terminal sequence. cathepsin b (CTSB) gene.

<400> 30

```

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gaatggcaca cctactggc tgg ttgccaa ctccctggaac actgactggg gtgacaatgg 120
cttcttttaa atactcagag gacaggatca ctgtggaatc gaatcagaag tgggtggctgg 180
aattccacgc accgatcagt actgggaaaa gatctaattc gccgtgggcc tgcgtgccca 240
gtcctggggg gcgagatcgg ggtagaaatg cattttatct ttttaagttc cgtaaggat 300
acaagtttct agacagggtc tgaaagggan tgggatttng gccaaacatc agacctgttc 360
tttcccaagg gaggaccaag ttctgggct aacattcccc agcctnttgg ttttaacagtt 420
gncagacag ggcctgtt 439

```

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<210> 31
<211> 1996
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1996)
<223> cathepsin b (CTSB) gene.

<400> 31
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tttttgaaaa attacagctt caccctgtca agttaacaag gaatgcctgt gccataaaaa 1980
ggtttctcca acttga 1996

<210> 32
<211> 492
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(492)

21/292

<223> 3' terminal sequence. protein phosphatase 4
(formerly x), catalytic subunit (PPP4C) gene.

<400> 32

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aacaaaacaga aaaaagaagg aaaaaaagaa aaaaaaatta ttggaaactt catggttcaa 120
gtggggagag aggaggagga acatggagct aggtctccag gcctctccag agaagtcctc 180
accctcgaag caccctcttg ggggacagca gagccagg ga cagccccccc ccacgccag 240
cctccgtctg aggaagatg ggcagagtca cagtgggtgc gaggggccag aagggttggg 300
aggngggcag gggcgggagg ggtcacagga agtagttcgg ccacggcttt ctttgggagg 360
gggatncccc gtgtcttctt ttgggggagc agccttcaaa gatgatgaaa tctttttctt 420
gggagatgct tcgttc cagc ttnccaagat tggcttncca cattttcca cagcgggtaca 480
agttagtttt tg                                         492
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<210> 33

<211> 330

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(330)

<223> 5' terminal sequence. protein phosphatase 4
(formerly x), catalytic subunit (PPP4C) gene.

<400> 33

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ctggcactta aggttcgcta tcctgategc atcacactga tccgggg caa ccatgagagt 120
cgccagatca cgcaggtcta tggcttctac gatgagtgcc tgcgcaagta acggctcggg 180
gactgtgtgg cgctactgca ctgagatctt tgactacctc agcctgtcag ccatcatcga 240
tngaaagaat cttctgcgtg cacggggggc tctccccctc catccagacc ctgggatcca 300
gattcggaca atcgaccgaa agcaa gaggt                                         330
```

<210> 34

<211> 1429

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1429)

<223> protein phosphatase 4 (formerly x),
catalytic subunit (PPP4C) gene.

<400> 34

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gagggggcgg cggccccgac tctgaccgc gccgggggtg ggccatggcg gagatcagcg 120
acctggaccg gcagatcgag cagctgcgtc gctgcgagct catcaaggag agcgaagtca 180
aggeccctgtg cgctaaggcc agagagatct tggtagagga gagcaacgtg cagagggtgg 240
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tcagagtagg tggcgacgtc cctgagacca actacctctt catgggggac tttgtggacc 360
gtggcttcta tagcgtcgaa acgttcctcc tgctgctggc acttaagggt t cgctatcctg 420
atcgcatcac actgatccgg ggcaaccatg agagtcgcca gatcacgcag gtctatggct 480
```

22/292

```

tctacgatga gtgcctgcgc aagtacggct cggtgactgt gtggcgctac tgcactgaga 540
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gcctctcccc ctccatccag accctgg atc agattcggac aatcgaccga aagcaagagg 660
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ctaataaaag aagaaaaatg aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1380
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1429

```

<210> 35

<211> 493

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(493)

<223> 3' terminal sequence. ests (EST T79867)
gene.

<400> 35

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tcccttcccc aagctagctt tggaa taaat ccacttttct tgtaccagac cccactcttg 120
ttaattggac tctacatgtg gnaagcaact aacttgattt tcggttacaa tataatattc 180
aacttcagta aatcaaagac aattttgaaa gaagccaaag ggaaaaaat gacctgaaga 240
gtcctgttta anttttagatt tctgaacaca aatctctggc gactaggact gaagcttgac 300
ctnttctctac ccaggaccn ttcccacctc actagggnac tttggantgg gatatatgtg 360
gggaaactct tgggctttcc ccattgtggc accatttcat atcttatggc aaatggtgcc 420
tcctacctcc cttgggnac tcccngttg gatgggnttt gggggaggag nctgntggg 480
gntttttccc at 493

```

<210> 36

<211> 354

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(354)

<223> 3' terminal sequence. fibroblast growth
factor receptor 4 (FGFR4) g ene...

<400> 36

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tttttgtttt ttatttcaaa aaaataattt ataaaacgcc atttgctcct gttttcggca 60
ggcttccagc ttctctgggc tcaggggcaa tgctcccgtc aagacgtggt ggcagcagca 120

```

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gcagggggag gtnntggggaa aggggggttca gaggcccaga acctcctgct ggtattggga 180
ggcaggagggt ttagcatagc agctctcca g ccaggctcag ccaaaccgg gatggggact 240
aagcgccaag gtccaagaag ccgagcagaa ccctgacatt tggggccatc aggacanagg 300
cacggcagct cccaaggga aggggcacgg ccttngggac angggcacag caac 354

<210> 37

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(336)

<223> 5' terminal sequence. fibroblast growth
factor receptor 4 (FGFR4) gene.

<400> 37

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ggcagcagcg ccctcccaga ggcctacct caagcagctg gtgaggcgc tggacaaggt 120
ctgctggccg tctctgagga gtacctcgac ctccgcctga ccttcggacc ctattcccc 180
tctggtggg aacgccagca gcacctgctt cctccagcga ttctgtcttc agccacgacc 240
ccctgccatt ggggattcag ctccctccct ttgggtctng ggggtgcagac atga gcaagg 300
ctnaagggtt ttgcaaggga catagggttg gtgggc 336

<210> 38

<211> 3015

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3015)

<223> fibroblast growth factor receptor 4 (FGFR4)
gene.

<400> 38

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agtccagctt gggccctga gactgtgag aaggagatgc ggctgctgct gg ccctgttg 180
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cccctcctgc aggcggggct cccggccaac accacagccg tgggtggcag cgacgtggag 960
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24/292

```

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```

3015

<210> 39

<211> 252

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(252)

<223> 3' terminal sequence. ectonucleotide
pyrophosphatase/phosphodiesterase 2 (autotaxin)
(ENPP2) gene.

<400> 39

```

gtgtgattta ttatgtttaa gattggttta taaggcttaa atatctctgt catagttaac 60
agttaacagc aaataaaggc aactttacaa aatcagtggt tccatacagt acaggactaa 120
atgtggcaac tgtgcattgg aaaattaata ttctcctaat gcaaatntca aatctgcagc 180
accatttaga agcttccact aaaaactcaa gctgcagtat ttattacang ctctactcng 240
aacacanggc ta

```

252

<210> 40

<211> 382

25/292

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(382)

<223> 5' terminal sequence. ectonucleotide
pyrophosphatase/phosphodiesterase 2 (autotaxin)
(ENPP2) gene.

<400> 40

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gaaagaaatg gagttaacgt gataagtga ccaatcttcg actatgacta tgatggctta 120
catgacacag aagacaaaat aaaacagtac gtggaaggca gttccattcc tgttccaact 180
cactactaca gcatcatcac cagctgtctg gatcttactc agcctgccga caagtgtgac 240
ggccctctct ctgtgtcttc cttcatcctg cctcaccggc ctgacaacga ggagagctgc 300
aatagctcag aggacgnatt caaaatgggt agnaggaact catgaaggnt gcacacagct 360
agggtncgtt gacctttgna cc                                     382
```

<210> 41

<211> 2592

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2592)

<223> ectonucleotide
pyrophosphatase/phosphodiesterase 2 (autotaxin)
(ENPP2) gene.

<400> 41

```
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ggagtcaata tctgcttagg attcaactgca catcgaatta agagagcaga aggatgggag 120
gaaggtcctc ctacagtgtc atcagactcc ccctggacca acatctccgg atcttgcaag 180
ggcaggtgct ttgaacttca agaggctgga cctcctgatt gtcgctgtga caacttgtgt 240
aagagctata ccagttgctg ccatgacttt gatgagctgt gtttgaagac agcccgtgcg 300
tgggagtgtg ctaaggacag atgtggggaa gtcagaaatg aagaaaatgc ctgtcactgc 360
tcagaggact gcttggccag gggagactgc tgtaccaatt accaagtggg ttgcaaagga 420
gagtcgcatt gggttgatga tgactgtgag gaaataaagg ccgcagaatg ccc tgcaggg 480
tttgttcgcc ctccattaat catcttctcc gtggatggct tccgtgcac atacatgaag 540
aaaggcagca aagtcatgcc taatattgaa aaactaaggc cttgtggcac acactctccc 600
tacatgaggc cgggtgtacc aactaaaacc tttcctaact tatacacttt ggccactggg 660
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gctaaatatg accccaaagc cattattgcc aatctcacgt gtaaaaaacc agatcagcac 1260
ttaagcctt acttgaaaca gcaccttccc aaacgtttgc actatgcaa caacagaaga 1320
```

26/292

```

attgaggata tccatttatt ggtg gaacgc agatggcatg ttgcaaggaa acctttggat 1380
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gtcaacagca tgcagactgt tttttaggt tatggcccaa catttaagta caagactaaa 1500
gtgcctccat ttgaaaacat tgaactttac aatgttatgt gtgatctcct gggattgaag 156 0
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gacaacgagg agagctgcaa tagctc agag gacgaatcaa aatgggtaga agaactcatg 2460
aagatgcaca gcagtagggt gcgtgacatt gaacatctca ccagcctgga cttcttccga 2520
aagaccagcc gcagctaccc agaaatctg acactcaaga catacctgca tacatatgag 2580
agcgagattt aa 2592

```

<210> 42

<211> 467

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(467)

<223> 3' terminal sequence. v-rel avian
reticuloendotheliosis viral oncogene homolog a
(nuclear factor of kappa light polypeptide gene
enhancer in b-cells 3 (p65)) (RELA) gene.

<400> 42

```

acagatttat tagttcagag tagaaagagc aagagtccaa gtgctttgat tgttcagtaa 60
aaactatgcc tccngactgg agagctgcca gcctgctctc cccactctt aacaacttac 120
cctactatta aggcaactga gaagagggag agcaagggaag tcccagacca aacccttct 180
ggatccnggg ngagagccag tgctgttgcn tggtnntcct tcagccatgg ttgagcaagg 240
aaagagccgg cagagacctc ttagggcag gaaggccagc ccctcaaacg ctggtnttag 300
ggcacagggg acaatgccag tgccatacag gggctggtat ctgggggcgt tattttgatt 360
aagctgtaat gaatccatga tgggaaggac acttgataag gctttntggg gctcaaaggn 420
ctttacctcc agcctgcttc tntctctagg gngagtaccc agaagct 467

```

<210> 43

<211> 2444

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2444)

<223> v-rel avian reticuloendotheliosis viral
oncogene homolog a (nuclear factor of kappa light
polypeptide gene enhancer in b-cells 3 (p65))
(RELA) gene.

<400> 43

```
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gtcccgcggg cagcatccca ggagagagga gcacagatac caccaagacc caccaccacca 180
tcaagatcaa tggctacaca ggaccaggga cagtgcgcat ctccctgggc a ccaaggacc 240
ctcctcaccg gcctcaccac cagcagcttg taggaaagga ctgccgggat ggcttctatg 300
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tgaagaagcg ggacctggag caggctatca gtcagcgcac ccagaccaac aacaacccct 420
tccaagttcc tatagaagag cagcgtgggg actacgacct gaatgctgtg cggctctgct 480
tccaggtgac agtgcgggac ccatcaggca ggccccctcg cctgccgcct gtcctttctc 540
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gaaactcttg cagctgcctc ggtggggatg agatcttct actgtgtgac aaggtgcaga 660
aagaggacat tgaggtgtat ttacggggac caggctggga ggcccagggc tccttttctc 720
aagctgatgt gcaccgacaa gtggccattg tgttccggac cctccctac gcagaccca 780
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aactaataaa gctgttgcca agctggacgg cagcagctcg tgcc 2444
```

<210> 44

<211> 381

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(381)

28/292

<223> 5' terminal sequence. il2 -inducible t-cell
kinase (ITK) gene.

<400> 44

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ggatcatgaa caactttatc ctcttggaag aacagctcat caagaaatcc caacaagaga 120
agaacttctc cctcgaactt taaagtccgc ttctttgtgt taaccaaagc cagcctgg ca 180
tactttgaag atcgatcatgg gaagaagcgc acgctgaagg ggtocattga gctctcccga 240
attcaaatgt gttgaggttg tgaagaagtga catcagcatc ccatgccact attaaatacc 300
cgttttcagg tnggtgcatg acaacttacc tcctnttatg gtgtttgntt ccagntcgtg 360
aggaggccgg ncagcgttng g                                     381
```

<210> 45

<211> 6381

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(6381)

<223> il2-inducible t-cell kinase (ITK) gene.

<400> 45

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aatatattca acacttacaa aaagtatat gataaagaat ataaagtact agtttccttt 180
taacacttca aaagatatgt atatatactt ttttttaca gtaacatcac aaatgctcac 240
atcttcacat gctcttaaaag tattatttgt actcagtgtg aggctattat cgtttttcat 300
acataaaaatt ttctagctct gtaacacaat gcaattttta atccattcag taagttcaac 360
cccaaaagtg ccgcttccca gcattaagac atgcacccac ccctcttcta agattttcta 420
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atggctgaca ttagtagcaa aaccttagtt atctgaaaat aacatattgg aaatgagaca 540
ttattaggat tttaaacaaa caatagcatt tagacataaa gtaggaagca aaatacagta 600
aacagaaata gtgtagcaa atatcattct cttcagctac cttagtaaa agacaaaaca 660
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caggtgagct ttggtcagtc tgttcttcaa aatatgtatg atcatatggt aatgaagttt 1200
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```

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30/292

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ctgtacagcc tgacactgta tgggctgcga ggacccaca agggcgacag catccaggga 11580
accgcccga ccctcagccc agttctggag agccccctg acctccaatt cagtgaatc 11640

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```

agggagacct cagccaaggt caactggatg cccccacat cccgggcgga cagcttcaaa 11700
gtctcctacc agctggcgga cggaggggag cctcagagtg tgcagggtga tggccag gcc 11760
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accttcacca cagggtaga ggccctcgg gacttggagg ccaaggaagt gacccccgc 1218 0
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```

<210> 48

<211> 438

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(438)

<223> 3' terminal sequence. colony stimulating factor 1 (macrophage) (CSF1) gene.

<400> 48

```

ttttgcagct tgtgcacttc ttttattatt aaatatataa gcagcttccat atcttttaaa 60
tagatatitaa aatgacttta tataaaataa ttcaccactt ccaagtataa aaacaaaatc 120
tcacagtgcg tgancaatgt cctctc ttga cttctcagag aacagaagg gttcctgagc 180
aggtagcctg gggggacacc agaggngcct ctggggctcc tctgctctg atgccaccaa 240
gtgctcaaaa agagcttctg cagtggggtt gggattgctt ttttgacctt taaaatatta 300
tatgtttaag gtagggggg atgaagggg gaatgccctt tttatttttc ttccattttt 360
aaaaatatgt gttttctagg catccaaata tagggggctg tggcctggga gggctaggcc 420
ccctttgccca ggttctact 438

```

<210> 49

<211> 390

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(390)

<223> 5' terminal sequence. colony stimulating factor 1 (macrophage) (CSF1) gene.

<400> 49

```
ggcagcaggc gagctctgac tgaagatggg cctttgaaat ataggtatgc acctgaggtt 60
gggggagggt ctgcactccc aaaccccagc gcagtgtcct ttccctgc tg ccgacagaac 120
ctggggctga gcaggttata cctgtcagga gccctgggac tgggctgcat ctacgcccac 180
cctggcatgg tatccagctc ccattccatt ctccaccctt ctttcctcct gaccttgggt 240
caacagtgat ggaccttcca actcttcacc caccctctct accattcacc tctaaaccag 300
gggaagccag gggtngggag agcant cagg gagagccagg gcttcagttt tccaattgct 360
ggggangggc ttccattttt tggggccagc 390
```

<210> 50

<211> 2475

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2475)

<223> colony stimulating factor 1 (macrophage) (CSF1) gene.

<400> 50

```
agccgctctc cgcattcccag gacagcgggtg cggccctcgg ccggggcgcc cactccgcag 60
caccagcgca ggcagcgagc gagcgagggc ggccgacgcg ccgggcccgg acccagctgc 120
ccgtatgacc ggcgggggag ccggccgggc ctgccctccc acgacatggc tgggtccctt 180
gctgtgtgtg gtctgtctcc tggcgagcag gagtatcacc gaggaggtgt cggagtactg 240
tagccacatg attgggagtg gacacctgca gtctctgcag cggtgattg acagtcagat 300
ggagacctcg tgccaaatta catttgagtt ttagaccag gaacagttga aagatccagt 36 0
gtgctacctt aagaaggcat ttctcctggt acaagacata atggaggaca ccattgcgctt 420
cagagataac acccccattg ccattcgccat tgtgcagctg caggaaactct ctttgaggct 480
gaagagctgc ttaccaaagg attatgaaga gcatgacaag gcctgcgtcc gaactttcta 540
tgagacacct ctccagttgc tggagaaggc caagaatgtc tttaatgaaa caaagaatct 600
ccttgacaag gactggaata ttttcagcaa gaactgcaac aacagctttg ctgaatgctc 660
cagccaagat gtggtgacca agcctgattg caactgcctg taccctaaag ccattccctag 720
cagtgaacctg gcctctgtct cccctcatca gccctcgcgc ccctccatgg ccctgtgtgc 780
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acatgagagg cagtccgagg gatctccag ccgcagctc caggagtctg tcttccacct 1620
gctggtgccc agtgtcatcc tgggtcttgc ggccgtcggg ggcctcttg t tctacaggtg 1680
```

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```
gaggcgggcg agccatcaag agcctcagag agcggattct cccttgagc aaccagaggg 1740
cagccccctc actcaggatg acagacaggt ggaactgccg gtgtagaggg aattctaaga 1800
cccctcacca tcttgacac tctcgtttgt caatgtccct ctgaaaatgt gacgcccagc 1860
cccgacaca gtactccaga tgttgtctga ccagctcaga gagagtacag tgggactgtt 1920
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gatgtagctg tgacctatt gtccctcacc cctgccc ccc gccaaccca gctggcccac 2340
ctcttcccc tcccaccaa gccacagcc agccatcag gaagccttc tggcttctcc 2400
acaaccttct gactgtctt tcagtcagc ccctgctct tttgtattg gctaatagta 2460
tatcaatttg cactt                                     2475
```

<210> 51

<211> 397

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(397)

<223> 3' terminal sequence. villin 2 (ezrin)
(VIL2) gene.

<400> 51

```
atcngttgaa tagttgatc catacatttc cagg tcttga gcaatcttca ggtattccaa 60
catagcatta tctttgagca tcccacggtg ttccgcatgc cacacctgga tccggtcctc 120
ccactggtcc ctggttaagt tgtgctggtc catcactctt tgagggatca nccgctcaga 180
gctgaggtag ccagacttgt gcacttcttt gttgtagtcc ccaaacttgg cctgcacagc 240
gtagggaccc caagagcacg gcagtctcag ggggggcagt agatctcatc gctaagggat 300
tcttttctt cacttnggag ggaggaaaag tttctggggt gatgtcctgg ggatgagctt 360
ccttcagcca catcttccag ggnaggact ttnggcc                                     397
```

<210> 52

<211> 468

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(468)

<223> 5' terminal sequence. villin 2 (ezrin)
(VIL2) gene.

<400> 52

```
ggacgaggca gggcgggcg ggcctctaag ggttctgctc tgactccagg ttgggacagc 60
gtcttcgctg ctgctggata gtcgtgtttt cggggatcga ggatactcac cagaaaccga 120
aaatgccgaa accaatcaat gtccgagtta ccaccatgga tgcagagctg gagtttgcaa 180
tccagccaaa tacaactgga aaacagcttt ttgatcaggt ggtaaagact atcggcctcc 240
gggaagtgtg gtactttggc ctccactatg tggatnaata aaggatttcc tacctgg gct 300
gaagctggat aagaaggtgt ctgcccagga ggtcaggaag gagaatcccc tccagttcaa 360
```

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gttccggggc caagtcttac cctgaagatg tgggctgagg agctcattcc agggacattc 420
acccagaaat tttntttcnt ccaagtgaag gaagggttc ttaggcgn 468

<210> 53

<211> 3064

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3064)

<223> villin 2 (ezrin) (VIL2) gene.

<400> 53

aggcaggggc ggcggggcgt ctaagggttc tgctctgact ccagggtggg acagcgtctt 60
cgctgctgct ggatag tcgt gttttcgggg atcgaggata ctcaccagaa accgaaaatg 120
ccgaaaccac tcaatgtccg agttaccacc atggatgcag agctggagtt tgcaatccag 180
ccaaatacaa ctggaaaaca gctttttgat caggtggtaa agactatcgg cctccgggaa 240
gtgtgggtact ttggcctcca ctatgtggat aataaaggat ttccctacctg gctgaagc tg 300
gataagaagg tgtctgcccc ggaggtcagg aaggagaatc ccctccagtt caagttccgg 360
gccaagttct accctgaaga tgtggctgag gagctcatcc aggacatcac ccagaaactt 420
ttcttctctc aagtgaagga aggaatcctt agcgatgaga tctactgcc ccctgagact 480
gccgtgctct tggggctcta cgctgtgcag gccaaag ttg gggactacaa caaagaagtg 540
cacaagtctg ggtacctcag ctctgagcgg ctgatccctc aaagagtgat ggaccagcac 600
aaacttacca gggaccagtg ggaggaccgg atccagggtg ggcattgcga acaccgtggg 660
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atacacctta ttaatgatca gctatatact atttatatac aagtgataat acagatttgt 2580

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```
aacattagtt ttaaaaaggg aaagttttgt tctgtatatt ttgttacctt ttacagaata 2640
aaagaattac atatgaaaaa ccctctaaac catggcactt gatgtga tgt ggcaggagg 2700
nagtgggtgga gctggacctg cctgctgcag ctgcagtcac gtgtaaacag gattattatt 2760
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gccactcoat tccttctcgt gcactgcttt ctccttcaca gctaagatgc catgtgcagg 3000
tggattccat gccgcagaca tgaaataaaa gctttgcaaa ggcaaagaaa aaaaaaaaaa 3060
aaaa 3064
```

<210> 54

<211> 435

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(435)

<223> 3' terminal sequence. adenomatosis polyposis
coli (APC) gene.

<400> 54

```
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gataacagca atatatcata ttttctatct gtagtggtca ttattttaag acaagcaata 120
attaaaggaa gttgggatgg gatgctactt taaatacatg taaaacatac tgtacaaaca 180
tacttggtct tactattttt ttctaacca tcaagagtgc ctcccaaat aa gnccagtg 240
aagacaaagt atactatcaa atatgggctt ccnggaacaa aaacctctt aacaaggnt 300
ccaaacccta ttaccacaaa tttcccggt cttttaaggt ttccatttgg aaaccacaaat 360
gtctatatgg ccggttggtg attancatgg ggnttttctt ggnttccctt cttccnccct 420
cttttaacc ggtgg 435
```

<210> 55

<211> 414

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(414)

<223> 5' terminal sequence. adenomatosis polyposis
coli (APC) gene.

<400> 55

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tgggtgtgaa tcaaagactc taatttatca aatggcacct gctgtttcta aaacagagga 120
tgtttgggtg agaattgagg actgtcccat taacaatcct agatctggaa gatctccac 180
aggtaatact ccccggtgga ttg acagtgt ttcagaaaag gcaaatccaa acattaaaga 240
ttcaaaagat aatcagggca aaacaaaatg tggggtaatn ggcagtgttc ccatgncgta 300
ccgtggggtt tnggaaaatc gcctggaact cctttatttc aggtgggatg cccctgacca 360
aaaaggganc ttnnggttna aaccggggnc aaattattcc tgttccctgt tttc 414
```

<210> 56

<211> 10383

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(10383)

<223> adenomatosis polyposis coli (APC) gene.

<400> 56

```
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aagataattc caatcatctt acaaaactgg aaactgaggc atctaataatg aaggaagtac 180
ttaaacaact acaaggaagt attgaagatg aagctatggc ttcttctgga cagattgatt 240
tattagagcg tcttaaagag cttaacttag atagcagtaa tttccctgga gtaaaactgc 300
ggtcacaaaat gtcctccgt tcttatggaa gccgggaagg atctgtatca agccgttctg 360
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gagaaagtac tggatattta gaagaacttg agaaagagag gtcattgctt ctgc tgatc 480
ttgacaaaga agaaaaggaa aaagactggt attacgctca acttcagaat ctactaaaa 540
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cagccagtggt tttgagttct agtagcacac actctgcacc tcgaaggctg acaagtcac 960
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cat 10383

<210> 57
<211> 404
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(404)
<223> 5' terminal sequence. mucin 1, transmembrane
(MUC1) gene.

<400> 57
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tgctggtctg tggtctggtt gcgctggcca ttgtctatct cattgccttg gctgtctgtc 180
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ctatgagcga gtaccccacc taccacaccc atggggcgct atgtgcccc taggcagtac 300
cgatcgtagc ccctatgaga aggtttttng caggtaatng gttggcagca gcttttttta 360
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<210> 58
<211> 1721
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1721)
<223> mucin 1, transmembrane (MUC1) gene.

<400> 58
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acaggttctg gtcattgcaag ctctaccoca ggtggagaaa aggagacttc ggctaccag 180
agaagttcag tgcccagctc tactgagaag aatgctgtga gtatgaccag cagcgtactc 240
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caattgactc tggccttccg agaaggtacc atcaatgtcc acgacgtgga gacacagttc 1200
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<210> 59

<211> 359

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(359)

<223> 3' terminal sequence. insulin-like growth factor 2 (somatomedin a) (IGF2) gene.

<400> 59

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atgtgaaggg tgtttaagc caatcgattt tgtacatgtt tgaagatgct gctgtgcttc 240
ctcagcccga tggagggggc cgaggagagt agcctgtttc ggggaggcng ggcacgggga 300
ctgggtcang agaagcccca gggggaccgt ngacccaga gattttcggg atggaacc 359

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<210> 60

<211> 410

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(410)

<223> 5' terminal sequence. insulin-like growth factor 2 (somatomedin a) (IGF2) gene.

<400> 60

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gatgggccag caatcggaag tgagcaaat tgccgcaagt nttcagccc ggcgncacca 300
ttccttgag cttntntntt gaaccacgga gtttttctn aggtttccat tcngaaaa t 360
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<210> 61
<211> 1356
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1356)
<223> insulin-like growth factor 2 (somatomedin a)
(IGF2) gene.

<400> 61
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ctccccccct cagcccgcc ctctcgctt cgccgaacca aagtggatta attacacgct 120
ttctgtttct ctccgtgctg ttctctcccg ctgtgcgctt gcccgctctt cgctgtcttc 180
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ccgaaaagta caacatctgg cccgccccag cccgaagaca gcccgctctc cctggacaat 360
cagacgaatt ctccccccc ccccaaaa aa aaaagccatc cccccgctct gcccgctcgc 420
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<210> 62
<211> 474
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(474)
<223> 3' terminal sequence. egf-like module
containing, mucin-like, hormone receptor-like
sequence 1 (EMR1) gene.

<400> 62
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gcgtatgata ggcgctggag gggcacgctt agaaccatgc accaacaagg gcaggagaaa 120
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tctggaattg aagaagttgc aganaccgaa gataaaatgg tcgtttggag cagaaacacc 240
tgatttctca tcagtgcata caaccacagg aagacggccc ccaacatt ct tccccagagg 300

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<210> 63
<211> 457
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(457)
<223> 5' terminal sequence. egf-like module
containing, mucin-like, hormone receptor-like
sequence 1 (EMR1) gene.

<400> 63
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<210> 64
<211> 3149
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3149)
<223> egf-like module containing, mucin-like,
hormone receptor-like sequence 1 (EMR1) gene.

<400> 64
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<210> 65

<211> 412

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> misc_feature

<222> (1)..(412)

<223> 3' terminal sequence. k1aa0427 gene product
(K1AA0427) gene.

<400> 65

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412

<210> 66
<211> 442
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(442)
<223> 5' terminal sequence. kiaa0427 gene product
(KIAA0427) gene.

<400> 66
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<210> 67
<211> 5737
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(5737)
<223> kiaa0427 gene product (KIAA0427) gene.

<400> 67
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49/292

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<210> 68

<211> 377

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(377)

<223> 3' terminal sequence. spleen tyrosine kinase
(SYK) gene.

<400> 68

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aaattcacca caggcca 377
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<210> 69

<211> 323

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(323)

<223> 5' terminal sequence. spleen tyrosine kinase
(SYK) gene.

<400> 69

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50/292

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<210> 70

<211> 2541

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2541)

<223> spleen tyrosine kinase (SYK) gene.

<400> 70

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ggccatgaga ctgatccctg gccactgaaa agctttcctg aca ataaaaa tgttttgagg 2520
ctttaaaaag aaaaaaaaaa a 2541

<210> 71
<211> 312
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(312)
<223> 5' terminal sequence. interleukin 7 receptor
(IL7R) gene.

<400> 71
taacatcttt gtaagaaacc aagaaaaaat ttaaattgtga gtttcaatcc tgaaagtttc 60
ctggactgcc agattcatag ggtggatgac attcaagcta gagatgaagt ggaaggtttt 120
ctgcaagata cgtttctctca gcaactagaa gaatctga ga agcagaggct tngaggggat 180
gtgcagagcc ccaactgccc atctgaggat gtagtcatca ctccaggaaa gctttgggaa 240
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tttctcttt t
312

<210> 72
<211> 1658
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1658)
<223> interleukin 7 receptor (IL7R) gene.

<400> 72
ctctctctct atctctctca gaatgacaat tctagggtaca acttttggca tggt tttttc 60
tttacttcaa gtcgtttctg gagaaagtgg ctatgctcaa aatggagact tggaagatgc 120
agaactggat gactactcat tctcatgcta tagccagttg gaagtgaatg gatcgagca 180
ttcactgacc tgtgtctttg aggaccaga tgcacacacc accaatctgg aatttgaaat 240
atgtggggcc ctggtggagg taaagtgcct gaa tttcagg aaactacaag agatatattt 300
catcgagaca aagaaattct tactgattgg aaagagcaat atatgtgtga aggttggaga 360
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taaaggcttc tggagtgaat ggagtccaag ttattacttc agaactccag aga tcaataa 720
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cgctctgttg gtcattcttg cctgtgtgtt atggaaaaaa aggattaagc ctatcgtatg 840
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gggtcagccc attcttactt ccctgggac aaatcaagaa gaagca tatg tcaccatgtc 1380
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aattagcaaa accccactac acagtctgca agattctgaa acattgcttt gaccactctt 1560
cctgagttca gtggcactca acatgagtca agagcatcct gcttctacca tgtggatttg 1620
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<210> 73

<211> 236

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(236)

<223> 3' terminal sequence. v-myc avian
myelocytomatosis viral oncogene homolog (MYC)
gene.

<400> 73

taaaaacaat agaaaaaaat caactttaaa aagcaaaatg tacttaaata aaaaaaatta 60
gggtttatag tacctataat actaggnact atatactagg attgaaa ttc tgtgtaactg 120
ctataaacgt tttattaaag ttatttacat ttaatgggca atatttacag aggaaacatt 180
gtgtaaatct taaaattttt taaaanccaa ttcttaaata ccaaatctgt taaggg 236

<210> 74

<211> 413

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(413)

<223> 5' terminal sequence. v-myc avian
myelocytomatosis viral oncogene homolog (MYC)
gene.

<400> 74

acgtctccac acatcagcac aactacgcag cgcctccctc cactcggaag gactatcctg 60
ctgccaaagag ggtcaagttg gacagtgtca gagtcctgag acagatcagc aacaaccgaa 120
aatgcaccag cccaggtcc tcggacaccg aggagaatgt caagaggcga acacacaacg 180
tcttgggagc gccagaggag gaacgagcta aaacggagct tttttgccct gcgtgaccag 240
atcccggagt tgggaaaaca atgaaaaggc cccaaggta gttattcctt taa aaaagcc 300
acagcntaca tcctgttccg ttccaaggca ggagggagcc aaaagttcat tttnttgaag 360
gagggntttt tttccgggn aacgaagagg aaccatttn aaacacaant ttt 413

<210> 75

<211> 2121

<212> DNA/RNA

<213> Artificial Sequence

<220>

53/292

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2121)

<223> v-myc avian myelocytomatosis viral oncogene
homolog (MYC) gene.

<400> 75

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cggaactctt gtgcgtaagg aaaagtaagg aaaacgattc cttctaacag aaatgtcctg 1920
agcaatcacc tatgaacttg tttcaaatgc atgatcaaat gcaacctcac aacctgggt 1980
gagtcttgag actgaaagat ttagccataa tgtaaaactgc ctcaaattgg actttgggca 2040
taaaagaact tttttatgct taccatcttt ttttttctt taacagattt gtatttaaga 2100
attgttttta aaaaatttta a 2121
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<210> 76

<211> 260

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(260)

<223> 3' terminal sequence. gata-binding protein 3
(GATA3) gene.

54/292

<400> 76

tcacagcact agagaccctg ttaaataagg gatatgagtc agaattggctt attcacagat 60
gggtgccaga ttcaagtgggtt ggaacacaga caccacagtg agctcctttg caaagtggca 120
aacataattt tgctttctgc cttcaaaaac atatatccat cgcgttttagg cttcatgata 180
ctgctcctgc aaaaatgcaa gtcgaaaggg actgcaggga ctctcgtgg ggggccctgt 240
gagcatcgag cagggtcttt 260

<210> 77

<211> 409

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(409)

<223> 5' terminal sequence. gata-binding protein 3
(GATA3) gene.

<400> 77

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tctggtttct tcaacttcctt ataagggcac caatcttatt cagagggtc tcaccctcga 120
aataatcacg tctcaaaaac cccacacctc taatattcta ataccatcac gtgagggtt 180
aggtttcaac ataagaattc ggtggtggtt ggggtngggg gagagggaaa caaacatcca 240
gaccagaaac cgaaaaatgt ctagcaaatc caaaaagtgc aaaaaagt gc atgactcact 300
ggaggacttc cccaagganc agctnctgtt taaccggggc cgcccttttc caggacacat 360
gttccttccc tggnggccac atnttgncc ttnaggccan tccaggga 409

<210> 78

<211> 2365

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2365)

<223> gata-binding protein 3 (GATA3) gene.

<400> 78

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ggcaggagcc ccccgacctc ccaggcggac cgcccttccc tccccgcgag ggttccgggc 120
cggcgagag ggcgcgacga cagccgaggc catggagggtg acggcggacc agccgcgctg 180
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cctcagccac tctacatgg acgcggcgca gtaccgcgtg ccggaggagg tggatgtgct 300
ttttaacatc gacggtcaag gcaaccacgt ccgcacctac ta cggaaact cggtcagggc 360
cacggtgcag aggtacctc cgaccacca cgggagccag gtgtgccgcc cgctctgct 420
tcattgatacc ctaccctggc tggacggcg caaagccctg ggcagccacc acaccgcctc 480
cccttgaat ctcagccctt tctccaagac gtccatccac caccgctccc cggggccct 540
ctcgtctac ccccgccct cgtcctctc cttgtcgggg ggccacgcca gccgcacct 600
cttcaccttc ccgcccaccc cgccgaagga cgtctcccc gaccatcgc tgtccacccc 660
aggctcggcc ggctcggccc ggcaggacga gaaagagtgc ctcaagtacc aggtgccct 720
gcccgacagc atgaagctgg agtcgtccca ctcccgtggc agcatgacc ccctgggtgg 78 0
agctcctcg tcgacccacc accccatcac cacctaccgc ccctacgtgc ccgagtacag 840
ctccgactc ttcccccca gcagcctgct gggcggtcc cccaccggct tcggatgcaa 900

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gtccaggccc aaggcccggt ccagcacagg cagggagtgt gtgaactgtg gggcaacctc 960
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acagggcccc cagcgagagt ccctgcagtc cctttcgact tgcatTTTTT caggagcagt 1560
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ttatacagac cgaactgttg tataaattta tttactgcta gtcttaagaa ctgctttctt 2280
tcgtttgttt gtttcaa tat tttccttctc totcaatttt cggttgaata aactagatta 2340
cattcagttg gcaaaaaaaa aaaaa 2365
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<210> 79

<211> 328

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(328)

<223> 3' terminal sequence. growth factor
receptor-bound protein 7 (GRB7) gene.

<400> 79

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ctcggctctgt acaaagtgtg gggcgtgaaa ccgctgggct gccccactt ctcccataat 120
tccctgccct agagcagcag ctccagagct aggagaagga gagggggcca cccaaggcct 180
tcccttgagg agaggggtca ggagtggact ggagtggggg ctgttttcta tctgaggag 240
gcaaagaagc agaggagaaa actggagtgg cggaaccctc ccgntcctca tcccgtcccc 300
tgtggccgat cccanagtcc actnggat 328
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<210> 80

<211> 428

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(428)

56/292

<223> 5' terminal sequence. growth factor
receptor-bound protein 7 (GRB7) gene.

<400> 80

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ggctccccac ctttgagaag tgctcagat aataccctgg tggccatgga cttctctggc 60
catgctgggc gtgtcattga gaacccccgg gaggtcttga gtgtggccct ggaggaggcc 120
caggcctgga ggaagaagac aaaccaccgc ctacgctgc ccatgccagc ctccggacga 180
gcctcagtgc agccatccac cgcacccaac tctgggtcca cgggcgcat tccgtgagg 240
agagccagcg tttattggga cagcagggtc tngtagacgg cctgttctg ggtccgggag 300
agtcagcggg aacccccagg ggtttttcct cttttnttg ccacctgca gaaagtgaag 360
cnttattttc attccttgcc gagcgaagga ggaagggccg cttttatttt aagcattggt 42 0
tgattggc 428
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<210> 81

<211> 2205

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2205)

<223> growth factor receptor-bound protein 7
(GRB7) gene.

<400> 81

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tgtagagaag cgggagtgga tctgaaataa aatccaggaa tctgggggtt cctagacgga 120
gccagacttc ggaacgggtg tctgtctact cctgctgggg ctctccagg acaaggga c 180
acaactggtt ccgttaagcc cctctctcgc tcagacgcca tggagctgga tctgtctcca 240
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cccaaccctt tccctgagct ctgcagtcct ccctcacaga gccaattct cggggggccc 480
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acgcgggtgg ccctctgacc aggcggtgga ctggctcatg cctcagcccg ccttcaggct 1860
gcccgcggcc cctccacca tccagtggac tctggggcgc ggccacaggg gacgggatga 1 920
```

57/292

ggagcgggag ggttcgcca ctccagtttt ctctctgct tctttgcctc cctcagatag 1980
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 tgggggcagc ccaggcggtt tcacgcccga cacttt gtac agaccgagag gccagttgat 2160
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<210> 82

<211> 313

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(313)

<223> 5' terminal sequence. topoisomerase (dna) ii
 beta (180kd) (TOP2B) gene.

<400> 82

gaaatttgac agtaatgaag aagattctgc ttctgttttt tcaccatcat ttggtctgaa 60
 acagacagat aaagtccaa gtaaaacggg agctgctaaa aagggtatgt acttataattt 120
 gattgagtta agcattgg at agagatagtt aatgtaaaag gaaatgtaat ttaatttgaa 180
 actatttgca tttttttatc ataaaacaat taagggaagta taagtgccta taaggaggac 240
 ctctcgtttt ctagccatct gagggcggtta ataaatttct gtaggactta ntttaaagct 300
 gttgtanttt taa 313

<210> 83

<211> 4866

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4866)

<223> topoisomerase (dna) ii beta (180kd) (TOP2B)
 gene.

<400> 83

atggccaagt cgggtggctg cggcgcgggga gccggcggtg gcggcgggcaa cggggcactg 60
 acctgggtga acaatgctgc aaaaaaagaa gagtcagaaa ctgccacaa aaatgattct 120
 tcaaagaagt tgtctgttga gagagtgtat cagaagaaga cacaacttga acacattctt 180
 ctctgcctcg atacatata tgggtcagtg gagccattga cgcagttcat gtgggtgt at 240
 gatgaagatg taggaatgaa ttgcaggag gttaccttg tgccaggttt atacaagatc 300
 tttgatgaaa ttttggttaa tgctgctgac aataaacaga gggataagaa catgacttgt 360
 attaaagtgt ctattgatcc tgaatctaac attataagca tttggaataa tgggaaaggc 420
 attccagtag tagaacacaa gtagagaaa gtttat gtgc ctgctttaat tttggacag 480
 cttttaacat ccagtaacta tgatgatgat gagaaaaaag ttacagggtg tcgtaatggt 540
 tatggtgcaa aactttgtaa tattttcagt acaaagttaa cagtagaac agcttgcaa 600
 gaatacaaac acagttttaa gcagacatgg atgaataata tgatgaagac ttctgaagcc 660
 aaaattaaac attttgatgg tgaagattac acatgcataa cattccaacc agatctgtcc 720
 aaatttaaga tggaaaact tgacaaggat attgtggccc tcatgactag aagggcata 780
 gatttggctg gttcgtgtag aggggtcaag gtcattgtta atggaaagaa attgcctgta 840
 aatggatttc gcagttatgt agatctttat gtgaaagaca aattggatga aactgg ggtg 900
 gccctgaaag ttattcatga gcttgcaaat gaaagatggg atgtttgtct cacattgagt 960

gaaaaaggat tccagcaaat cagctttgta aatagtattg caactacaaa aggtggacgg 1020
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 aacaaagctg gtgtatcagt gaaaccattt ca agtaaaaa accatatatg ggtttttatt 1140
 aattgcctta ttgaaaatcc aacttttgat tctcagacta aggaaaacat gactctgcag 1200
 cccaaaagtt ttgggtctaa atgccagctg tcagaaaaat tttttaagc agcctctaatt 1260
 tgtggcattg tagaaaagtt cctgaactgg gtgaaattta aggtcagac tcagctgaat 1320
 aagaagtgtt catcagtaaa atacagtaaa atcaaaagga ttcccaaact ggatgatgct 1380
 aatgatgctg gtggtaaaaca ttccctggag tgtacactga tattaacaga gggagactct 1440
 gccaaatcac tggctgtgtc tggattaggt gtgattggac gagacagata cggagttttt 1500
 ccactcaggg gcaaaattct taatgtacgg gaagcttctc ataaac agat catggaaaat 1560
 gctgaaataa ataattattat taaaatagtt ggtctacaat ataagaaaag ttacgatgat 1620
 gcagaatctc tgaaaacott acgctatgga aagattatga ttatgaccga tcaggatcaa 1680
 gatggttctc acataaaaag cctgcttatt aatttcattc atcacaattg gccatcactt 1740
 ttgaagcatg gttttcttga agagttcatt actcctattg taaaggcaag caaaaataag 1800
 caggaacttt ccttctacag tattcctgaa tttgacgaat ggaaaaaaca tatagaaaac 1860
 cagaaagcct ggaaaaataaa gtactataaa ggattgggta ctagtacagc taaagaagca 1920
 aaggaatatt ttgctgatat ggaaagcat cgcattctgt ttagatatgc tggctctgaa 1980
 gatgatgctg ccattacott ggcathtagt aagaagaaga ttgatgacag aaaagaatgg 2040
 ttaacaaatt ttatggaaga ccggagacag cgtaggctac atggcttacc agagcaattt 2100
 ttatatggta ctgcaacaaa gcatttgact tataatgatt tcatcaacaa ggaattgatt 2160
 ctcttctcaa actcagacaa tgaaagatct atac catctc ttgttgatgg ctttaaacct 2220
 ggccagcgga aagttttatt tacctgtttc aagaggaatg ataaacgtga agtaaaagt 2280
 gccagttgg ctggctctgt tgcctgagat tgcgcttctc atcatggaga acaagcattg 2340
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 cagcctattg gtcagtttgg aactcggctt catggtggca aagatgctgc aagccctcgt 2460
 tatattttca caatgttaag cacttttagc aggtactttt ttctgtctgt ggatgacaac 2520
 ctcttttaag tctttatga tgataatcaa cgtgtagagc ctgagtggtg ttttctata 2580
 attcccatgg ttttaataaa tgggtgctgag ggcattggta ctggatgg gc ttgtaaaacta 2640
 cccaactatg atgctagggg aattgtgaac aatgtcagac gaatgctaga tggcctggat 2700
 cctcatccca tgcttccaaa ctacaaaaac tttaaaggca cgattcaaga acttggtcaa 2760
 aaccagtatg cagtcagtgg tgaaatattt gtagtggaca gaaacacagt agaaattaca 2820
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 aatggaacag ataaaaacac agcattaatt tctgattata aagaatatca tactgacaca 2940
 actgtgaaat ttgtgtgaa aatgactgaa gagaactag cacaagcaga agctgctgga 3000
 ctgcataaag tttttaaaact tcaaaactact cttacttgta attccatggt actttttgat 3060
 catatgggat gtctgaagaa atatgaaact gtgcaagaca ttctgaaaga attctttgat 3120
 ttacgattaa gttattacgg tttacgtaag gagtggcttg tgggaatgtt gggagcagaa 3180
 tctacaaagc ttaacaatca agcccgtttc atttttagaga agatacaagg gaaaattact 3240
 atagagaata ggtcaaagaa agatttgatt caaatg ttag tccagagagg ttatgaattc 3300
 gaccagtgta aagcctggaa agaagcaca gaaaaggcag cagaagagga tgaaacacaa 3360
 aaccagcatg atgatagttc ctccgattca ggaactcctt caggcccaga ttttaattat 3420
 atttttaata tgtctctgtg gtctcttact aaagaaaaag ttgaagaact gattaaacag 3480
 agagatgcaa aagggcgaga ggtcaatgat cttaaaagaa aatctccttc agatctttgg 3540
 aaagaggatt tagcggcatt tggtagaaga ctggataaag tggaaatctca agaacgagaa 3600
 gatgttctgg ctggaatgac tggaaaagca attaaaggta aagttggcaa acctaaagg 3660
 aagaaactcc agttggaaga gacaatgcc tcaccttatg gcagaagaat aattcctgaa 3720
 attacagcta tgaagcaga tgccagcaaa aagttgctga agaagaaga gggatgatt 3780
 gatactgcag cagtaaaagt ggaatttgat gaagaattca gtggagcacc agtagaagg 3840
 gcaggagaag aggcattgac tccatcagtt cctataaata aaggtcccaa acctaaagg 3900
 gagaagaagg agcctgttac caga gtgaga aaaacaccta catcatctgg taaacctagt 3960
 gcaagaaaag tgaagaaacg gaatccttgg tcagatgatg aatccaagtc agaaagtgat 4020
 ttggaagaaa cagaacctgt ggttattcca agagattctt tgcttaggag agcagcagcc 4080
 gaaagaccta aatacacatt tgatttctca gaagaagagg atgatgatgc tgatgatgat 4140
 gatgatgaca ataagattt agagaaattg aaagttaaa catctccat acaaatgat 4200
 ggggaagatg aatttgttcc ttcagatggg ttgataaag atgaatatac attttcacca 4260
 ggcaaatcaa aagccactcc agaaaaatct ttgcatgaca aaaaaagtca ggattttgga 4320
 aatctcttct catttcttcc atattctcag aagtcaga ag atgattcagc taaatttgac 4380
 agtaatgaag aagattctgc ttctgtttt tcaccatcat ttggtctgaa acagacagat 4440
 aaagttccaa gtaaaacggg agctgctaaa aagggaaaac cgtcttcaga tacagtcctt 4500
 aagcccaaga gagcccaaaa acagaagaaa gtagtagagg ctgtaaactc tgactcggat 4560
 tcagaatttg gc attccaaa gaagactaca acacaaaag gtaaaggccg aggggcaaa 4620

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aaaaggaaag catctggctc tgaaaatgaa ggcgattata accctggcag gaaaacatcc 4680
aaaacaacaa gcaagaaacc gaagaagaca tcttttgatc aggattcaga tgtggacatc 4740
ttcccctcag acttccctac tgagccacct tctctgccac gaaccggtcg g gctaggaaa 4800
gaagtaaaat attttacaga gtctgatgaa gaagaagatg atgttgattt tgcaatgttt 4860
aattaa 4866

<210> 84

<211> 311

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(311)

<223> 3' terminal sequence. caspase 4,
apoptosis-related cysteine protease (CASP4) gene.

<400> 84

cactttttatt gaaatacaaaa atgttaaata tgcaagctgt actaatgaag gtgctccttg 60
aagttgatta aggagggtcg ggctgcttgg ggcttccatt ttcaattgcc aggaaagagg 120
tagaaatatac ttgtcatgga cagtcgttct atgggtggga tttgagcttt ggcccttgga 180
gtttcaaatg attgctgtac cttccgaaat acttctctta ggtggcagca ccaagaatat 240
ttctgggaag catgtgatga gttgtgtgat gaagatagag cccattgtg ctgtctctcc 300
cagggcacgt t 311

<210> 85

<211> 1291

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1291)

<223> caspase 4, apoptosis-related cysteine
protease (CASP4) gene.

<400> 85

gctctttcca acgctgtaaa aaaggacaga ggctgttccc tatggcagaa ggcaaccaca 60
gaaaaaagcc acttaagggtg ttggaatccc tgggcaaaga tttctcact ggtgttttgg 120
ataacttggg ggaacaaaat gtactgaact ggaaggaaga ggaaaaaag aa atattacg 180
atgctaaaaac tgaagacaaa gttcgggtca tggcagactc tatgcaagag aagcaacgta 240
tggcaggaca aatgcttctt caaacctttt ttaacataga ccaaatatcc cccaataaaa 300
aagctcatcc gaatatggag gctggaccac ctgagtcagg agaattctaca gatgccctca 360
agctttgtcc tcatgaagaa ttcttgagac tatgtaaaga aagagctgaa gagatctatc 420
caataaagga gagaaacaac cgcacacgcc tggctctcat catatgcaat acagagtttg 480
accatctgcc tccgaggaat ggagctgact ttgacatcac agggatgaag gagctacttg 540
agggctctgga ctatagtgtg gatgtagaag agaattctgac agccaggat atggagtcag 600
cgctgagggc atttgctacc agaccagagc acaagtcctc tgacagcaca ttcttggtac 660
tcatgtctca tggcatcctg gagggaatct gcggaactgt gcatgatgag aaaaaaccag 720
atgtgctgct ttaatgacac atcttccaga tattcaaca ccgcaactgc ctgagtcgta 780
aggacaaaacc caaggtcatc attgtccagg cctgcagagg tgcaaacctg ggggaactgt 840
gggtcagaga ctctccagca tccttggaag tggcctcttc acagtcattc gagaacctgg 900
aggaagatgc tgtttacaag acccacgtgg agaaggactt cattgctttc tgctcttcaa 960

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```
cgccacacaa cgtgtcctgg agagacagca caatgggctc tatcttcac acacaactca 1020
tcacatgctt ccagaaatat tcttggtg ct gccacctaga ggaagtattt cggaaggtag 1080
agcaatcatt tgaaactcca agggccaaag ctcaaagcc caccatagaa cgactgtcca 1140
tgacaagata tttctacctc tttcctggca attgaaaatg gaagccacaa gcagcccagc 1200
cctccttaat caacttcaag gagcaccttc attagtacag cttgcatatt taacattttg 1260
tatttcaata aaagtgaaga caaaaaaaaaa a 1291
```

<210> 86

<211> 319

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(319)

<223> 5' terminal sequence. tissue inhibitor of
metalloproteinase 2 (TIMP2) gene.

<400> 86

```
tggacccatg ggatgagtg tttattcatg ctgtttccag gaagggatgt cagagctgga 60
ccagtcgaaa cccttgaggg ctttttttgc agttggccac aggggctgtg gaggcctgct 120
tatgggtcct cgatgtcgag aaactcctgc ttgnggaacn ccgcg ccgcg tnnccacgca 180
caggagccnt cacttctctt gatgcaggcg aagaacttgg cctggnnccc gttnatgttc 240
ttctctgtga cccagtcocat ccagaggcac tcgtccgggg agganatgta gcacgggatc 300
atngggcanc gcgtgatct 319
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<210> 87

<211> 1075

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1075)

<223> tissue inhibitor of metalloproteinase 2
(TIMP2) gene.

<400> 87

```
cgcagcaaac acatccgtag aaggcagcgc ggccgccga g agccgcagcg ccgctcgccc 60
gccgcccccc acccgcgcgc ccgcgccgcg gaattgcgcc ccgcgcccct cccctcgcg 120
ccccgagaca aagaggagag aaagtgttgc cggccgagcg gggcaggtga ggagggtgag 180
ccgcgcggga ggggccccgc tcggccccgc ctcagcccc gccgcgcgcc ccagccccgc 240
gccgcgagca gcgcccgc ac cccccagcgc cggccccgc ccgcccagcc ccccgccccg 300
ccatgggcgc cgcggcccgc accctgcgcg tggcgtcgcg cctcctgctg ctggcgacgc 360
tgcttcgccc ggccgacgcc tgcagctgct ccccggtgca cccgcaacag gcgttttgca 420
atgcagatgt agtgatcagg gccaaagcgc tcagtggaga ggaagtggac tctggaaacg 480
acatttatgg caaccctatc aagaggatcc agtatgagat caagcagata aagatgttca 540
aagggcctga gaaggatata gattttatct acacggcccc ctctcggca gtgtgtgggg 600
tctcgctgga cgttgaggga aagaaggaat atctcattgc aggaaggcc gagggggacg 660
gcaagatgca catcacctc tgtgacttca tcgtgccc tg ggacaccctg agcaccaccc 720
agaagaagag cctgaaccac aggtaccaga tgggctgcga gtgcaagatc acgcgctgcc 780
ccatgatccc gtgctacatc tcctccccgc acgagtgcct ctggatggac tgggtcacag 840
agaagaacat caacgggcac caggccaagt tcttcgcctg catcaagaga agtgacggct 900
```

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cctgtgcgtg gtaccgcggc gggcgcccc ccaagcagga gtttctcgac atcgaggacc 960
cataagcagg cctccaacgc ccctgtggcc aactgcaaaa aaagcctcca agggtttcga 1020
ctggtccagc tctgacatcc ctctctggaa acagcatgaa taaaacactc atccc 1075

<210> 88
<211> 225
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(225)
<223> 3' terminal sequence. d -dopachrome
tautomerase (DDT) gene.

<400> 88
ttttttgaat gaggaagctc ttttcattta tttcanatga ggatgaagaa gaggattatg 60
tgancacagg aatnttgcag gcgggataat ccaaagctgg ttatctccag gncctcantn 120
tgccaagaga tctctctgga agaagcagcc agttcacaga tgccctggat ccctccgtgc 180
ccaatcataa aaaagtcag accgtcccta tnttgccaat ntgcc 225

<210> 89
<211> 312
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(312)
<223> 5' terminal sequence. d -dopachrome
tautomerase (DDT) gene.

<400> 89
cgttcctgga gctggacacg aatttgcccg ccaaccgagt gcccgcggn tngagaaac 60
gactctgcgc cgccgctgcc tccatcctgg gcaaacctgc ggaccgctg aacgtgacgg 120
tacggcgagg cctggccatg gcgctgagcg ggtccaccga gccctgcgcg cagtgttcca 180
tctcctccat cggcgtagtg gggcaccgag agggacaacc gcagccacag cgcccatctc 240
ttttgagttt tttcaccaag gagctaagcc cctgccaggg acccgat ant tattccttt 300
ttttcccttt gg 312

<210> 90
<211> 666
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(666)
<223> d-dopachrome tautomerase (DDT) gene.

<400> 90

```
gatccccgtg ccagggaccc tgcccagttc caggcgtcgc ctaaccaga aacgactggg 60
cgccgcgtcc tggaaaggcc ccagcgacag gacatctgag gagctgtttc cgttcctctg 120
cccgccatgc cgttcctgga gctggacacg aatttgccc ccaaccgagt gcccgcgggg 180
ctggagaaac gactctgcgc cgccgctgcc tccatcctgg gcaaacctgc ggaccgcgtg 240
aacgtgacgg tacggccggg cctggccatg gcgctgagcg ggtccaccga gccctgcgcg 300
cagctgtcca tctcctccat cggcgtagt ggaccgcgg aggacaaccg cagccacagc 360
gccacttct ttgagtttct caccaaggag ctaccctgg gcc aggaccg gatacttata 420
cgctttttcc ccttgagtc ctggcagatt ggcaagatag ggacggtcac gactttttta 480
tgattgggca cggagggatc caggcatct gtgaactggc tgcttcttcc agagagatct 540
cttggcagag tgagggcctg gagataacca gctttggatt atcccgcag caacattcct 600
gtgatcacat aatcctcttc ttcctctca tatgaaataa atgaagagag ctctctcatt 660
caaaaa
```

666

<210> 91

<211> 443

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(443)

<223> 3' terminal sequence. prolactin (PRL) gene.

<400> 91

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gantttgatg tctctaagga gtcagttttt attttttaag aggagacctg ttacacccaa 60
gcatggattc aaaagagata caactaaaag aagcttgcaa tggaaaggat cattaaggac 120
cttctcagaa atagatgaaa tggatgtggg cttagca gtt gttgttggg atgattcggg 180
cacttcaggg agcttgagga taattgtoga ttttatgtga atccctgcgt aggcaatggg 240
agaggttata ataaggcagg aaaggcgag actcttcac agccatctgc aggggatggg 300
aagtccccga ccagacagg gtagatctca tttcttttg gttttcagg atgaacctgg 360
gcttgactat ccagcttcca tgnccctctt ggaagccctt ttggttttgc tccctcaatc 420
ttctacagct tttgggttag ggt
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443

<210> 92

<211> 243

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(243)

<223> 5' terminal sequence. prolactin (PRL) gene.

<400> 92

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gaagaatcgg aacatacagg ctttgatata aaaggtttat aaagccaata tctgggaaag 60
agaaaaccgt gagacttcca gatcttctct ggtgaagtgt gtttcctgca acgatcacga 120
acatgaacat caaaggatcg ccatgggaaa ggtccctcc tgctgctgct ggtgtttcaa 180
acctgctcct gtgccagagc gtgggcccc ttggcccatc tgtcccgnc gggcttgccc 240
gat
```

243

<210> 93
<211> 833
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(833)
<223> prolactin (PRL) gene.

<400> 93
aaacatgaac atcaaaggat cgccatggaa agggtccttc ctgctgctgc tgggtgtcaaa 60
cctgctgctg tgccagagcg tggcccccctt gcccatctgt cccggcgggg ctgcccgatg 12 0
ccagggtgacc cttcgagacc tgtttgaccg cgccgtcgtc ctgtccact acatccataa 180
cctctcctca gaaatgttca gccaattcga taaacgggtat acccatggcc gggggttcat 240
taccaaggcc atcaacagct gccacacttc ttcccttgcc acccccgaag acaaggagca 300
agcccaacag atgaatcaaa aagactttct gagcctgata gtcagcatat tgcgatcctg 360
gaatgagcct ctgtatcatc tggtcacgga agtacgtggt atgcaagaag ccccgaggc 420
tactctatcc aaagctgtag agattgagga gcaaaccaaa cggttcttag agggcatgga 480
gctgatagtc agccagggtc atcctgaaac caaagaaaat gagatctacc ctgtctggtc 540
gggacttcca tccctgcaga tggctgatga agagtctcgc ctttctgctt attataacct 600
gctccactgc ctacgcaggg attcacataa aatcgacaat tatctcaagc tcctgaagtg 660
cgaatcatc cacaacaaca actgctaagc ccacatccat ttcatctatt tctgagaagg 720
tccttaatga tccgttccat tgcaagcttc ttttagttgt atctcttttg aatccatgct 780
tgggtgtaac aggtctcctc ttaaaaaata aaaactgact cgtagagac atc 833

<210> 94
<211> 304
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(304)
<223> 3' terminal sequence. prolactin receptor
(PRLR) gene.

<400> 94
actaagcagt gtgcttttat ttcatgaac acatagtttt ataactaaca gcaaaaagta 60
aatctacaaa tcacagttag gaaacataat gatttgttct ggaatcagct gctggagaaa 120
gaggcaagtg gttaaaaatg gagcatgaaa ggagctggga gcttttagtag tgtcagtctg 180
actacattct tgaggcattt cacgtactct gtagtggtac ctgaagaaaa atcacatttt 240
aaccaatcat tccattagtc aagctatcag tgaaaggagt gtgtaaaaca tgcgggatcc 300
cggg 304

<210> 95
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(366)
<223> 5' terminal sequence. prolactin receptor
(PRLR) gene.

<400> 95
gaggtcattg agaagccaga gaatcctgaa acanccca cctggaaccc ccantgcata 60
agcatggaag gcaaaatccc ctatttncat gctggtggat ccaaagtgtc aacatggccc 120
ttaccacagc ccagccagca caacccaga tcctcttacc acaatattac tgatgtgtgt 180
gagctggtcg tgggccctgc aggtgcaccg gccactctgt tgaatgaagc aggtaaagat 240
gctttaaaat cctctcaaac cattaagtct agagangag g gnaaggcaac ccaggcagag 300
ggaggtagga aagcttccat tcttgagnac tgaccagggt tacgnctgg gttgcttgcc 360
ccaggg 366

<210> 96
<211> 2723
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2723)
<223> prolactin receptor (PRLR) gene.

<400> 96
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65/292

aacagagaga gaacagcggc aagcccaaga agcccgggac tcttgagaac aataaggagt 1920
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<210> 97

<211> 365

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(365)

<223> 3' terminal sequence. interleukin 2
receptor, beta (IL2RB) gene.

<400> 97

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aaataatcac aaagatggta cacacggatc attaaaagat acggatgtat aggatacata 180
tgtcacaat gattaaggac ttaaaaaatg taaccctccc aagaagtggg gagcctccca 240
aagtggggga agggcaaata caatttcnt ttgggggggg atagggngac cccctttgca 300
gagaggggtt aggtgggggt tcccccggn acacacaggc aagggtttgg gngccccttg 360
tgggg 365

<210> 98

<211> 366

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(366)

<223> 5' terminal sequence. interleukin 2
receptor, beta (IL2RB) gene.

<400> 98

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agggggtttg gcaccaagct ctgtccaatc aggtaggctg ggctgaacta gccaatcaga 120
tcaactctgt cttgggcgtt tgaactcagg gagggaggcc cttgggagca ggtgcttggtg 180
gacaaggctc cacaagcgtt gagccttgga aaggtagaca agcgttg agc cactaagcag 240
aggaccttgg gttcccaata caaaaatacc tactgctgag aggggntgct gaccattttg 300

66/292

gtcaaggatt tcngtttgcc ttatatccca aataaantcc cttttttttn aggtttnttt 360
agtntt 366

<210> 99

<211> 4034

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4034)

<223> interleukin 2 receptor, beta (IL2RB) gene.

<400> 99

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aactgaccac agttgacatc gtcaccctga ggtgctgtg ccgtgagggg gtgcgatgga 480
gggtgatggc catcaggac ttcaagccct ttgagaacct tcgctgatg gcccctatct 540
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67/292

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atctttgtta ctctgtaaat gaaaaaaccc attttcgcta taaataaaag gtaactgtac 4020
aaaataagta caat
4034

```

<210> 100

<211> 444

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(444)

<223> 3' terminal sequence. gata -binding protein 3 (GATA3) gene.

<400> 100

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aactggcagt ttgtccattt gaatatcaga cctagtttct tottaatttc cacacta ttt 120
ctcccatatt ccttaaacctt cttggcatcc ttcatgcctt acagctaccc agatgcaata 180
aagtcattgt acagtatttc ttacaatata agttatatgg caatgttcag gcattttttt 240
ttttcacagg cactaggagg accctgttta aatgggggat atgaggtcag gaatgggctt 300
attcacagga tgggggggtcc cggattcagg tgggt tgggg ancacaggac accacagggtg 360
aggctccctt tgccaaagggt ggggcaaac ataattttgg cttttctggc cttcaaaaa 420
catatttccn tcgcgttttg gggg
444

```

<210> 101

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

68/292

<221> misc_feature
<222> (1)..(396)
<223> 5' terminal sequence. gata-binding protein 3
(GATA3) gene.

<400> 101
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ccggccgccc tctccagaca catgtcctcc ctgagccaca tctcgccctt cagccactcc 240
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ccacaccacc cctccagctg ggtcacccgcc ntgggtttag agccttgtn gatggttcac 360
agggggcccc cagcgagagt tncctgnagt tccttt 396

<210> 102
<211> 416
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(416)
<223> 5' terminal sequence. placental growth
factor, vascular endothelial growth factor -related
protein (PGF) gene.

<400> 102
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acagactgcc acctgtgcgg cgatgctgtt ccccgagta acccaccct tggaggagag 120
agaccccgca cccggtcgt gtatttatta ccgtcacact ctacagtac tctgctggt 180
acctgccctc tatttattag ccaactgtt cctgtctgaa tgcctcgtc ccttcaagac 240
gaggggcagg gaaggacagg accctcagga attcagtgcc ttcaacaacg tga gagaaag 300
agagaagcca gccacagacc cctggggagc ttcccgctt tgaaagaagc aagacaagt 360
ggccttggt aggggcaagg ttagggccca ggaggccctn gggaagttt tcaggg 416

<210> 103
<211> 1645
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1645)
<223> placental growth factor, vascular
endothelial growth factor -related protein (PGF)
gene.

<400> 103
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tccccgggac ccgctgccc ctgcgcgcc cgccccgcg gccgctccc cgtcgggttc 120
cccagccaca gccttaccta cgggtcctg actccgcaag gcttcagaa gatgctcga 180
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1645

```

<210> 104

<211> 309

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(309)

<223> 5' terminal sequence. ubiquitin protein
ligase e3a (human papilloma virus e6 -associated
protein, angelman syndrome) (UBE3A) gene.

<400> 104

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ttcggcanag gggaaatgaa gcctgcacga atgagttttg tgcttcctgt ccaacttttc 60
ttcgtatgga taataatgca gc agctatta aagccctcga gctttataag antagggcaa 120
aactctgtga tcctcatccc tccaagaaag gagcaagctc agcttacctt gagaactcga 180
aaggtgcccc caacaactcc tgctctgaga taaaaatgaa caaggaaagg gcgctaggaa 240
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tccttggac
309

```

<210> 105

<211> 2628

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2628)

<223> ubiquitin protein ligase e3a (human

papilloma virus e6-associated protein, angelman
syndrome) (UBE3A) gene.

<400> 105

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gctagccgaa tgaagcgagc agctgcaaag catctaatag aacgctacta ccaccagtta 120
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gagatgatcg ctatggaaaa tcctgcagac ttgaagaagc agttgtatgt ggaatttgaa 1680
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ctggctatctt acaataactg tatactggat gtacattttc ccattggtgt ctacaggaag 1920
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gataaaattc caattacaaa tgaaaacagg aaggaatttg tcaatcttta ttctgactac 2160
attctcaata aatcagtaga aaaacagttc aaggcttttc ggagagggtt tcatatggtg 2220
accaatgaat ctcccttaaa gtacttattc agaccagaag aaattgaatt gcttatatgt 2280
ggaagccgga atctagat tt ccaagcacta gaagaaacta cagaatatga cggtggctat 2340
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ggaaaattaa agatgattat agccaaaaat ggcccagaca cagaaagggt acctaca tct 2520
catacttgct ttaatgtgct tttacttccg gaataactca gcaaagaaaa acttaaagag 2580
agattgttga aggccatcac gtatgccaaa ggatttggca tgctgtaa 2628
```

<210> 106

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence :primer

<220>

<221> misc_feature

<222> (1)..(363)

<223> 3' terminal sequence. oncogene tc21 (TC21)
gene.

<400> 106

```
aattttaatt ctagcacctg aagctatata agggatatgt ctataaactt catgggactg 60
tcgtacacac ttgataaagt gacaactgtg caataccact tagcatctca aaatcag gaa 120
catactattg aattgcttaa acacaatcca caganttaaa aacaaaatca ggatgccatc 180
cacagttata ctaattatcc attaaaaggc ttacacttaa tacttgaant aacaatcaat 240
atctagnccg ggnatactgg aaagtggatt tcagnnggtct catcctgttg gtactctatt 300
gggggngggg ttcttgaggt aggttatggt ggact gggnc caaggntggg ggggtaccacc 360
cag 363
```

<210> 107

<211> 408

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(408)

<223> 5' terminal sequence. oncogene tc21 (TC21)
gene.

<400> 107

```
gaattgaatc tacaaaagtg aaccatctca gacctttact gatactacaa cttttgtttt 60
ctgatggcca aaataccaaa tgcctgttgt atttatggat taaaaactgc ttataaaacc 120
ctgtgttact actcctactc ttggagatga taatattc ta tgtgggtcaaa tatttggact 180
catttaggac ttagatatct cagtgtactt gattttttta tttaactctt tttcacagcc 240
acgctaaggg taaaaaggaa taatttcctt ctgtcttcct tttcaagtat ttctgggtaa 300
gggattcaaa aaactaaaac tgtttttgtt tgtaataata aatatgggat tgatctttcc 360
ggggtcagag atgattaatg tttttgctat atacttttat acatgnnt 408
```

<210> 108

<211> 612

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(612)

<223> oncogene tc21 (TC21) gene.

<400> 108

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atggccgcgg cggctggcgg acggctccgg caggagaagt accggctcgt ggtggtcggc 60
gggggcggcg tgggcaagtc ggcgctcacc atccagttca tccagtccta ttttgaacg 120
gattatgac caaccattga agattcttac acaaagcagt gtgtgataga tgacagagca 180
gcccggttag atattttgga tacagcagga caagaagagt t tggagccat gagagaacag 240
tatatgagga ctggcgaagg cttcctgttg gtcttttcag tcacagatag aggcagtttt 300
gaagaaatct ataagtttca aagacagatt ctacagagta aggatcgtga tgagttccca 360
atgattttta ttgtaataa agcagatctg gatcatcaaa gacaggtaac acaggaagaa 420
ggacaacagt tagcacggca gcttaaggta acatacatgg aggcacagc aaagattagg 480
atgaatgtag atcaagcttt ccatgaactt gtccgggtta tcaggaaatt tcaagagcag 540
gaatgtcttc cttcaccaga accaacacgg aaagaaaaag acaagaaagg ctgccattgt 600
```


gtcattttct ag

6 12

<210> 109

<211> 592

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(592)

<223> 5' terminal sequence. tyrosine kinase with
immunoglobulin and epidermal growth facto r
homology domains (TIE) gene.

<400> 109

```
ngtcggagag aacctagcct ccaagattgc agacttcggc ctttctcggg gagaggaggt 60
ttatgtgaag aagacgatgg ggcgtctccc tgtgcgtgg atggccattg agtccctgaa 120
ctacagtgtc tataccacca agagtgtgtg ctggctcttt ggagtccttc ttggggagat 1 80
agtgaacctt ggaggtacac cctactgtgg catgacctgt gccgagctct atgaaaagct 240
gccccagggc taccgcatgg agcagcctcg aaactgtgac gatgaagtgt acgagctgat 300
gcgttcagtg ctggcgggac cgtccctatg agcgaccccc ctttgcccag attgcgctaa 360
cagctaggcc gcatgctggg aagccaggga aggcctatgt gaacatgttc gctgtttgag 420
aacttcaatt aacgcgggca ttgatgccac agctgaggag gnetgagctg ccatccagcc 480
agaactnggt ctgttgccg gagcaaat tttgtctaaa ctgtgaccag ttnaacctta 540
aagctttgat ttaagttgct taaggatttt ttaattaag ggagaaaaat tt 592
```

<210> 110

<211> 3845

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3845)

<223> tyrosine kinase with immunoglobulin and
epidermal growth factor homology domains (TIE)
gene.

<400> 110

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ttgctcccca tctcttctt ggcttctcat gtgggcgagg cggtggacct gacgctgctg 120
gccaacctgc ggctcacgga cccccagcgc ttcttcctga cttgcgtgtc tggggaggcc 180
ggggcgggga ggggtcggga cgcctggggc cc gcccctgc tgcctggagaa ggacgaccgt 240
atcgtgcgca ccccgcccg gcccaccctg cgcctggcgc gcaacggttc gcaccaggtc 300
acgcttcgcy gcttctccaa gccctcggac ctctgtggcg tcttctcctg cgtgggcggt 360
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ccagacaagg tcacacacac tgtgaacaaa ggtgacaccg ctgtactttc tgcacgtgtg 480
cacaaggaga agcagacaga cgtgatctgg aagagcaacg gatcctactt ctacaccctg 540
gactggcatg aageccaggga tgggcgggtc ctgctgcagc tcccaaatgt gcagccacca 600
tcgagcggca tctacagtgc cacttacctg gaagccagcc ccctgggcag cg ccttcttt 660
cggctcatcg tgcggggttg tggggctggg cgcctggggc caggctgtac caaggagtgc 720
ccaggttgcc tacatggagg tgtctgccac gaccatgacg gcgaatgtgt atgccccct 780
ggcttcactg gcaccgctg tgaacaggcc tgcagagagg gccgttttg gcagagctgc 840
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caggagcagt gccaggcat atcaggctgc cggggcctca ccttctgcct ccagacccc 900
tatggctgct cttgtggatc tggctggaga ggaagccagt gccaagaagc ttgtgccct 960
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384 5

<210> 111

<211> 202

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(202)
<223> 3' terminal sequence. autocrine motility
factor receptor (AMFR) gene.

<400> 111
aaagcccttc aaggtttact cncanctt gcaaggccca cancttggtc aaggaccaa 60
cccacaggtt ttagcactgc ctaatttact tcaccaatga atgaaaacca taaaccaaag 120
cttgctgcct aaccactccc cagggccaga cgggacaagg aaatgctgag aggggagggg 180
accatgggg canantnatg ag 202

<210> 112
<211> 450
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(450)
<223> 5' terminal sequence. autocrine motility
factor receptor (AMFR) gene.

<400> 112
attcaagtac cttttcctac acagcgggtca gatagcatca gacctgcatt gaacagtcct 60
gtggaaaggc caagcagtga ccaggaagag ggagaaactt ctgctcagac cgagcgtgtg 120
ccactggacc tcagtcctcg cctggaggag acgctggact tcggcgaggt ggaagtggag 180
cccagtgagg tggaagactt cgaggctogt gggagcgtt tctccaagtc tgctgatgag 240
agacagcgca tgtggtngca gcgtaaggac gaactcctcc agcaagctcg caaacgtttt 300
cttgaacaaa agttctgaag atgatgccgg ccttcagaga gctttcctnc ccttcggaaa 360
ggtgccgttc cttttgaacc ccgtgaacc ctnogttcg aaaggattgc ttggcttgcc 420
cgccgcggga aacggaggct ttcagaagca 450

<210> 113
<211> 1810
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1810)
<223> autocrine motility factor receptor (AMFR)
gene.

<400> 113
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gccactggac ctcagtcttc gcctggagga gacgtggac ttcggcgagg tggaagtgga 120
gcccagttag gtggaagact tcgaggctcg tggagcgc ttctccaagt ctgctgatga 180
gagacagcgc atgctggtcg cagcgtaagg acgaactcct ccagcaagct cgaaacgtt 240
tcttgaacaa aagtctgaa gatgatgcgg cctcagagag cttcctcccc tcggaagggtg 300
cgtcctctga ccccgtagc ctgcgtogaa ggatgctggc tgccgcgcgg aacggaggct 360
tcagaagcag cagacctcct agcgtccct tgcttctc agctgcct cc tgccgcctgt 420
gcccgaactga ctggaggagg cctgtcccaa ttctgccgt ccatggaaaa ggggcttga 480

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ctgcattgcc gctgtataaa gcatgtggtc ttatagtgtt tggacagctg ataaatttaa 540
tccttcctttg taatactttc tatgtgacat ttctcttccc cttagaaaca ctgcaaattt 600
taactgttagg tatgatctct tctggg gttg actggactgc ttgggggtggg ggacgatcag 660
gaggaagtga gccagtcgcc tgcctgcagc aggcagcttc tactcctgcc tcatgcatac 720
gtcccacaaa tgcaggtgtc ctgagcacca caccagtgga gaagagtgtg ggggaggcgc 780
acagtgtgag cccgccccca cgtcgtgggg taacatctgt tatcaaactg ctgtcgttgt 840
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cggaagttt ttagaatgtt gaaaagtaat tgaaaagggt gataggtaaa tttttaggca 1680
aagataattt atttcaataa atctttcaaa agc cttacct tgaaatgctg ttagtaaat 1740
tctgtgcatt tttttttttt aatttgttt gctgagagca tagctatttg tttttattgt 1800
aaaccgccc                                     1810

```

<210> 114

<211> 248

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(248)

<223> 3' terminal sequence. homo sapiens mrna;
 cdna dkfzp434c136 (from clone dkfzp434c136) (EST
 R81127) gene.

<400> 114

```

gaaattccaa aatcactcta gtttattcac ataatatagn atttgattcc attcttttgn 60
actgtgccn acttttaca tgtgtacaat gtttcacat gtnccaatta atgggtgagc 120
tttaaatgaa aatattctgg ancttccatt tatnggnatc aaccacaata gcaagacccc 180
cangaaatac ttgatctaaa ctgggagggt ccaacacaat tttttttttt aatgggnctt 240
gccacctt                                     248

```

<210> 115

<211> 415

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(415)

<223> 3' terminal sequence. b-cell cll/lymphoma 2
 (BCL2) gene.

<400> 115

ttttttaaag cagctttcga aatatcaacc acagcattaa acattgaaca gaggatattc 60
caaagttaat acagataaat ggtatataat gcaataatgc cacagagtta ttccatcaat 120
gtttcanggc tgattctaaa ctggangaaa aaaaaaattt cctagtttat ttgctganga 180
tgtcacttct tttgttactt ctttatagtt ccccaccatt gattttnttt ttaatgcccc 240
ggggtgtaca ggataacccc catattccac accgggggnac ttttttttg tcagggtttt 300
caaataaanc caaactacag tgacaggata atgttttaca ggtaattccn tgggcccggg 360
ggtcaattat nctgggacac ctcaattcaa ggntccttt gggggtttgg gggcc 415

<210> 116

<211> 468

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(468)

<223> 5' terminal sequence. b-cell cl1/lymphoma 2
(BCL2) gene.

<400> 116

aattgtgcca gaaaagcatt ttagcaattt atacaatatc atccagtacc ttaagccctg 60
attgtgtata ttcataatatt ttggatacgc accccccaac tccaataact ggctctgtct 120
gagtaagaaa cagaatcctc tggaacttga ggaagtgaac atttcggtga cttccgcac 180
aggaaggcta gagttaccca gagcatcagg ccgccacaag tgccctgctt t aggagaccg 240
aagtccgcag aacctgcctn tgtcccagct tggaggcctg gtccctgggaa ctgagccggg 300
gccctcactn gcctcctoca gggatgatca acaggngcag tgtggtntcc gaatgtctgg 360
aagcttgatg ggagctcaga atttccactg ttcaagaaag agncagtaga ggggtgtngc 420
tgggncctgtt cacttggggg ccctncaggt agngcccntt tttcacgt 468

<210> 117

<211> 6030

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(6030)

<223> b-cell cl1/lymphoma 2 (BCL2) gene.

<400> 117

gttggcccc gttacttttc ctctgggaaa tatggcgcac gctgggagaa cagggtacga 60
taaccgggag atagtatga agtatatcca ttataagctg tcgcagaggg gctacgagt 120
ggatgcggga gatgtgggag ccgcgcccc gggggccggc ccgcgcccgg gcatcttctc 180
ctcgcagccc gggcacacgc ccatacagc cgcatcccgg gacccg gtcg ccaggacctc 240
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tgccacggtg gtggaggagc tctt caggga cggggtgaac tgggggagga ttgtggcctt 480
ctttgagttc ggtggggtoa tgtgtgtgga gagcgtcaac cgggagatgt cggccctggt 540
ggacaacatc gccctgtgga tgactgagta cctgaaccgg cacctgcaca cctggatcca 600
ggataacgga ggctgggatg ctttgtgga actgtacggc cccagcatgc ggcctctgtt 660

tgattttctcc tggctgtctc tgaagactct gctcagtttg gccctggtgg gagcttgcat 720
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<210> 118

<211> 343

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(343)

<223> 5' terminal sequence. v-erb-b2 avian
erythroblastic leukemia viral oncogene homolog 2
(neuro/glioblastoma derived oncogene homolog)
(ERBB2) gene.

<400> 118

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<210> 119

<211> 4530

<212> DNA/RNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4530)

<223> v-erb-b2 avian erythroblastic leukemia viral
oncogene homolog 2 (neuro/glioblastoma derived
oncogene homolog) (ERBB2) gene.

<400> 119

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<210> 120

<211> 319

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(319)

<223> 5' terminal sequence. mouse double minute 2,
human homolog of; p53-binding protein (MDM2) gene.

<400> 120

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<210> 121

<211> 2372

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2372)

<223> mouse double minute 2, human homolog of;
p53-binding protein (MDM2) gene.

<400> 121

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<210> 122

<211> 343

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(343)

<223> 3' terminal sequence. gata-binding protein 3
(GATA3) gene.

<400> 122
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<210> 123
<211> 258
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(258)
<223> 3' terminal sequence. src homology 3
domain-containing protein hip-55 (HIP-55) gene.

<400> 123
cgagttagnt atgttgagg aacatgttgt gtctgccgtt ttggaatacc cagggtggga 60
gcttgccat ctgcatcccc acttcccata gcccaggcag agggac agag aaatggagtn 120
gggagcacag agcaggctcc aacaagacaa attccctgct gccaaaccac catgatccac 180
tctgactttg gncacaaact ctgctaaaaa caattctcta cgttcactgt tccaagggg 240
canttttaaa cagtgggtg 258

<210> 124
<211> 443
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(443)
<223> 5' terminal sequence. src homology 3
domain-containing protein hip-55 (HIP-55) gene.

<400> 124
gccagggctc agtgggcaag ggctctgtgc cgtgnocctg tacgactacc atgcagccga 60
cgacacagag atctcctttg accccgagaa cctcatcacg ggcacgagg tgatcgacga 120
aggctgggtg cgtggctatg ggccggatca tntgttngca tgttccctgc caactacgtg 180
gagctcattg agtgaggctg agggcacatc ttgcccttcc cctctcagac atggcttc ct 240
tattgctgga agaggaggcc tggggagtig acattcagca ctcttcagg gaataggggac 300
cccagttga ggattgagge ntcagggttc cctccggnnt gggcagattc agccttttca 360
ccccaaatgg cagcaattgg cntgggtgat ttcccaaaaa tcnttctg cttccccccg 420
acctttccca gacagtttg ttt 443

<210> 125
<211> 1331
<212> DNA/RNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1331)

<223> src homology 3 domain -containing protein
hip-55 (HIP-55) gene.

<400> 125

```
atggcggcga acctgagccg gaacgggcca gcgctgcaag aggcctacgt gcgggtggtc 60
accgagaagt ccccgaccga ctgggctctc ttacctatg aaggcaacag caatgacatc 120
cgcgtggctg gcacagggga ggggtgcctg gaggagatgg tggaggagct caacagcggg 180
aaggtgatgt acgccttctg cagagtgaag gaccccaact ctggactgcc caaatttgtc 240
ctcatcaact ggacaggcga gggcgtgaac gatgtgcgga agggagcctg tgccagccac 300
gtcagcacca tggccagctt cctgaagggg gccatgtga ccatcaacgc acgggcccag 360
gaggatgtgg agcctgagtg catcatggag aaggtggcca aggcttcagg tgccaactac 42 0
agctttcaca aggagagtgg ccgcttcacg gacgtgggac ccaggcccc agtgggctct 480
gtgtaccaga agaccaatgc cgtgtctgag attaaaaggg ttggtaaaga cagcttctgg 540
gccaaagcag agaaggagga ggagaaccgt cggtggagg aaaagcggcg ggccgaggag 600
gcacagcggc agctggagca ggagcgcggg gacgtgagc tgcgtgaggc tgcacgccgg 660
gagcagcgtc atcaggagca ggggtggcag gccagcccc agaggacgtg ggagcagcag 720
caagaagtgg tttcaaggaa ccgaaatgag caggagtctg ccgtgcacc gagggagatt 780
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ccagctgctg ccatctcaag gccagggca gatctccctg ctgaggagcc ggcccccagc 960
actcctcat gtctgtgca ggcagaagag gaggctgtgt atgaggaacc tccagagcag 1020
gagaccttct acgagcagcc cccactggtg cagcagcaag gtgccggctc tgagcacatt 1080
gaccaccaca ttcagggcca ggggtcagt gggcaagggc tctgtgccc tgccctgtac 1140
gactaccagg cagccgacga cacagagatc tcctttgacc ccgagaacct catcacgggc 1200
atcaggtga tgcaggaagg ctggtggcgt ggctatgggc cggatggcca ttttgcatg 1260
ttcctgccca actacgtgga gtcattgag tgag gctgag ggcggccgct agactagtct 1320
agagaaaaaa c 1331
```

<210> 126

<211> 430

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(430)

<223> 3' terminal sequence. cathepsin d (lysosomal
aspartyl protease) (CTSD) gene.

<400> 126

```
gtatttccat gtcagctggg gctctcagcc gccaagggg aggacaacag aggtcagctg 60
cagaggaagg ctggcaccag cccaatccc aacccacct ccaggccaat acatgccct 120
gggactggct cagtcccagc accaccctgc aggtccaac aaggtgggtt ttgtcccctc 180
tcaactcttc cagtcaccc tcaggcctct agcggcctca tctcaacgg gcccgggaca 240
ctgaacaggt aggtggggca gagccagctg ggncccaagc tnggcaagag gggccctcag 300
gcagggcagg ttttncagg gagggncctg gaggacggc ttgggtnttg g ggttaaggc 360
ttaanccagt cngggctttg gtaagggcc gnaagggat tccntgggna aattaaagg 420
aanccccagg 430
```

<210> 127

<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(339)
<223> 5' terminal sequence. cathepsin d (lysosomal
aspartyl protease) (CTSD) gene.

<400> 127
gtggatgagg tgcgcgactg cagaaggcca tcggggcgtn gccgctgatt cagggcgagt 60
acatgatccc ctgtgagaag gtgtccacc c tgcgcgcat cactactgaag ctgggaggca 120
aaggctacaa gctgtcccca gaggactaca cgctcaagggt gtgcgaggcc gggaagaccc 180
tctgcctgag cggcttcatg ggcatggaca tcccgccacc cagcggnac tctggatcct 240
ggggcgacgt cttcattcgg ccgttantac attgtgtttt gaccgtgaca acaacagggt 300
tgggtttcgc gaggcttgcc cgcttttagt ttcccaagg 339

<210> 128
<211> 1988
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1988)
<223> cathepsin d (lysosomal aspartyl protease)
(CTSD) gene.

<400> 128
ccatgcagcc ctccagcctt ctgcgcgtcg ccctctgcct gctggctgca cccgcctccg 60
cgctcgtcag gatcccgctg cacaagttca cgtccatccg cgggaccatg tcggagggtg 120
ggggctctgt ggaggacctg attgccaaag gcccgcgtctc aaagtactcc caggcggtgc 18 0
cagccgtgac cgaggggccc attcccgagg tgctcaagaa ctacatggac gccagttact 240
acggggagat tggcatcggg acgccccccc agtgcttcac agtcgtcttc gacacgggct 300
cctccaacct gtgggtcccc tccatccact gcaaaactgct ggacatcgct tgctggatcc 360
accacaagta caacagcgac aagtccagca cctaogttaa gaatggtacc tcgtttgaca 420
tccactatgg ctccggcagc ctctccgggt acctgagcca ggacactgtg tcggtgcctt 480
gccagtcagc gtgcgtcagc tctgccctgg gcggtgtcaa agtgagagg caggtctttg 540
gggaggccac caagcagcca ggcacacact tcatcgagc caagttcgat ggcacccctg 600
gcattggccta ccccgcatc tccgtcaaca acgtgctgcc cgtcttcgac aacctgatgc 660
agcagaagct ggtggaccag aacatcttct ccttctacct gagcaggac ccagatgcgc 720
agcctggggg tgagctgatg ctgggtggca cagactccaa gtattacaag ggttctctgt 780
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gcccgacttg ctgttttgtt ctgtgtgttt cccctccctg ggttcagaaa tgctgcctgc 1440

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ggaggtgggg ttgggattgg gggctggtgc cagccttcct ctgcagctga cctctgttg 1920
cctccccttg ggcggctgag agccccagct gacatggaaa tacagttgtt ggcctccgc 1980
ctcccctc 1988
```

<210> 129

<211> 385

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(385)

<223> 5' terminal sequence. insulin -like growth
factor 1 receptor (IGF1R) gene.

<400> 129

```
gtggcggcac tcattgttct cgggtcacgc ccgttccca caogtgcttg tggcacattt 60
tctggcagcg gtttgtggtc cagcagcggg agttgtactc at tgttgatg gtggtcttct 120
cacacatcgg cttctcctcc atgttccctg gacacaggtc cccacattcc tttgggggct 180
tattcccac aatgtagtta ttggacaccg catccaggat cagggaccag tccacagtng 240
agaggttaaca gaggtcagca tttttctcaa tcctgatggc ccccgagta atgttctca 300
ggttgtaaaag cccaatatcc ttgaggatgg gtcaatcttc gaaggatgaa ccaggggcnt 360
aggtttnttg gaaggagntt ttcca 385
```

<210> 130

<211> 4989

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4989)

<223> insulin-like growth factor 1 receptor
(IGF1R) gene.

<400> 130

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tttttttttt ttttgagaaa gggaatttca tcccaaataa aaggaatgaa gtctggctcc 60
ggaggagggt cccgcacctc gctgtggggg ctccgttttc tctccgcgc gctctcgtc 120
tggccgacga gtgga gaaat ctgcgggcca ggcatcgaca tccgcaacga ctatcagcag 180
ctgaagcgcc tggagaactg cacggtgatc gagggctacc tccacatcct gctcatctcc 240
aaggccgagg actaccgcag ctaccgcttc cccaagctca cggtcattac cgagtacttg 300
ctgctgttcc gagtggctgg cctcgagagc ctoggagacc tcttcccaa cctcagc gtc 360
atcccgggct ggaaactctt ctacaactac gccctggtca tcttcgagat gaccaatctc 420
aaggatattg ggctttacaa cctgaggaac attactcggg gggccatcag gattgagaaa 480
aatgctgacc tctgttacct ctccactgtg gactgggtccc tgatcctgga tgcgggtgctc 540
aataactaca ttgtggggaa taagcccca aagga atgtg gggacctgtg tccagggacc 600
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atggaggaga agccgatgtg tgagaagacc accatcaaca atgagtacaa ctaccgctgc 660
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gagaacaatg agtgctgcca ccccgagtgc ctgggcagct gcagcgcgcc tgacaacgac 780
acggcctgtg tagcttgccg ccactactac tatgccggtg tctgtgtgcc tgccctgccg 840
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gagtgcacct cgggcttcat ccgcaacggc agccagagca tgtactgcat cctt gtgaa 1020
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gagagaactg tcatttctaa ccttcggcct ttacattgt accgcatcga tatccacagc 2460
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acctgctgat ccttgatcc tgaatctgtg caaacagtaa cgtgtgcgca cgcgcagcgg 4200
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```
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tgaaccggc 4989
```

<210> 131

<211> 470

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(470)

<223> 5' terminal sequence. insulin receptor
(INSR) gene.

<400> 131

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tctgattcga ggagagacct tggaaattng gaactactcc ttctatgcct tggacaacca 180
gaacctaaag cagctctggg actggagcaa acacaacctc accatcactc aggggaaact 240
cttcttccac tataaccca aactctgctt gtcagaaatc cacaagatgg gaaggaagtt 300
tcagggaacc aaggggncgc cagg aggaga aacgacattt nccctggaag gaccaatggg 360
gggaccaggg catcctgtgg aaaaatggag tttactttaa anttttgctt taacattngg 420
gacntttttt tggacaagtt ttttgttgaa gttggggagc cctnattttg 470
```

<210> 132

<211> 4691

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4691)

<223> insulin receptor (INSR) gene.

<400> 132

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tgattacttg ctgctcttcc ggggtctatgg gctcgagagc ctgaaggacc tgttcccaa 420
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cctcacgggtc atccgggggat caccgactgtt ctttaactac gcgctgggtca tcttcgagat 480
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89/292

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<210> 133

<211> 451

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(451)

<223> 5' terminal sequence. forkhead box ola
(rhabdomyosarcoma) (FOXO1A) gene.

<400> 133

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<210> 134

<211> 5723

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5723)

<223> forkhead box ola (rhabdomyosarcoma) (FOXO1A)
gene.

<400> 134

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5723

<210> 135

<211> 466

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(466)

<223> 3' terminal sequence. epidermal growth
factor receptor (avian erythroblasti c leukemia
viral (v-erb-b) oncogene homolog) (EGFR) gene.

<400> 135

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466

<210> 136

<211> 450

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(450)

<223> 5' terminal sequence. epidermal growth
factor receptor (avian erythroblastic leukemia
viral (v-erb-b) oncogene homolog) (EGFR) gene.

<400> 136

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<210> 137

<211> 5532

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5532)

<223> epidermal growth factor receptor (avian
erythroblastic leukemia viral (v-erb-b) oncogene
homolog) (EGFR) gene.

<400> 137

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94/292

```

agatgtttta gaaggaaaaa agtt ccttcc taaaataatt tctctacaat tggaagattg 5220
gaagattcag ctagttagga gccattttt tctaatctg tgtgtgccct gtaacctgac 5280
tggttaacag cagtcctttg taaacagtgt tttaaactct cctagtcaat atccacccca 5340
tccaatttat caaggaagaa atggttcaga aaatattttc agcctacagt tatgttcagt 540 0
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```

<210> 138
 <211> 378
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(378)
 <223> 3' terminal sequence. tek tyrosine kinase,
 endothelial (venous malformations, multiple
 cutaneous and mucosal) (TEK) gene.

```

<400> 138
ggatnagant ttanaggcaa gacatttatt cactcatgat atatcagtgc aaagtgtgcc 60
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catgtaggga tattaattca atatataaat gtcacatgtc tcccaaattgt caccaggt 180
ttctgttatt tcttaaaata tacaagtcaa t attaccaga gaaaagataa gaaaatccca 240
ttattttatc ctaaaacttat gtatacttct ctaaagattc ttagggcttg taagcaatga 300
ggtttaaggc natttttttag gatgttagca tcccggggct gacttngccg ggctgtggga 360
acccaggncc cggagtgg 378

```

<210> 139
 <211> 447
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(447)
 <223> 5' terminal sequence. tek tyrosine kinase,
 endothelial (venous malformations, multiple
 cutaneous and mucosal) (TEK) gene.

```

<400> 139
gctttcactg gcatgggaga cccttgacac ctgctgagaa aacatgcctc tgccaaagga 60
tgtgatatat aagtgtacat atgtgctgta cacctgggac cttcaccact gtagatccca 120
tgcattgata tatgtagtat gctctgactc taataggact gtatatactg ttttaagaat 180
gggctgaaat cagaatgcct gtttgtggtt tcatatgcaa taatatattt ttttaaaaat 240
gtggacttca taggaaggcg tgagtacaat tagtataatg cataactcat tgttgccta 300
ggatattttg atatttacct ttatgttga atgctattaa atgttttccn gtgtccaaag 360
taaaatattg ttttaataaac ctaacaatgg accccgatag tacag ggta agtgaggga 420
accttatgga ttctaacaag tcttagg 447

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<210> 140

<211> 4138
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(4138)
<223> tek tyrosine kinase, endothelial (venous
malformations, multiple cutaneous and mucosal)
(TEK) gene.

<400> 140
cttctgtgct gttccttctt gccctctaact tgtaaaacaag acgtactagg acgatgctaa 60
tggaagagca caaacgcgtg gggttttgaa aggatccttg ggacctcatg cac atttgtg 120
gaaactggat ggagagattt ggggaagcat ggactcttta gccagcttag ttctctgtgg 180
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gctggaagtt actcaagatg tgaccagaga atgggctaaa aaagttgttt ggaagagaga 420
aaaggctagt aagatcaatg gtgcttattt ctgtgaaggg cgagttcgag gagaggcaat 480
caggatacga accatgaaga tgcgtcaaca agcttccttc ctaccagcta ctttaactat 540
gactgtggac aaggagagata acgtgaacat atctttcaaa aaggtattga ttaaagaaga 600
agatgcagtg atttacaata atggttcctt catccattca gtgccccggc atgaagtacc 660
tgatattcta gaagtacacc tgcctcatgc tcagcccag gatgctggag tgtactcggc 720
caggtatata ggaggaaaacc tcttcacctc ggcttcacc aggctgatag t ccggagatg 780
tgaagcccag aagtggggac ctgaatgcaa ccactctctg actgcttgta tgaacaatgg 840
tgtctgccat gaagatactg gagaatgcat ttgcccctc gggtttatgg gaaggacgtg 900
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```

<210> 141

<211> 395

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(395)

<223> 3' terminal sequence. tumor necrosis factor
receptor superfamily, member 6 (TNFRSF6) gene.

<400> 141

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taattccaaa cacaaggggc aaaaaaatcc tccataaatg gaagttcttt aggtggttcc 60
aggnatctgc ttcagtttat aa ctatcttc acagtttaca tttacagaaa tataaatatt 120
atttcttaaa attcacattt aatacaaaact ttcaaagata tttaaacgta ggatagtagt 180
aaggagaatc ttaaattcta gaaacttggg ggtatgacaa gagcaattcc taaatccaga 240
tgatgatttt accattgcta tgtataagct gccatttgta ggcaggtttt acatggggac 300
attattgaac attttcgggg ggtgggggga aaaataaggn atctatttta tccatctttg 360
gattggcaaa cctgggggttc angacatgtt caciaa 395

```

<210> 142

<211> 461

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(461)

<223> 5' terminal sequence. tumor necrosis factor

receptor superfamily, member 6 (TNFRSF6) gene.

<400> 142

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tcgtaattgg catcaacttc atggaaagaa agaagcgtat gacacattga ttaaagatct 60
caaaaaagcc aatcttttga ctcttgcag a gaaaattcag actatcatcc tcaaggacat 120
tactagtgc tcagaaaatt caaacttcag aaatgaaatc caaagcttgg tctagagtga 180
aaaacaacaa attcagttct gagtatatgc aattagtgtt tgaaaagatt cttaatagct 240
ggctgtaaat actgcttggg tttttactgg gtacatttta tcatttatta gcgctgaaga 300
gccacatat ttgtagggtt ttaatatctc catggattct gcctccaagg gtgtttaaaa 360
tctagttggg ggaacaaac ttccttcaag ggttaaatgc ngtggcctgg ctaagtaccc 420
ccattaggga gtgtttgccg ggggttgnaa ggtttaggtt t 461
```

<210> 143

<211> 2551

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2551)

<223> tumor necrosis factor receptor superfamily,
member 6 (TNFRSF6) gene.

<400> 143

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gtgacttggc tggagcctca ggggcgggca ctggcacgga acacaccctg aggccagccc 120
tggctgcccc ggcgagctg cctcttctcc cgcggttgg tggaccgct cagtacggag 180
ttggggaagc tctttcactt cggaggattg ctcaacaacc atgctgggca tctggacct 240
cctacctctg gttcttacgt ctgttgc ag attatcgtcc aaaagtgtta atgcccaagt 300
gactgacatc aactccaagg gattggaatt gaggaagact gttactacag ttgagactca 360
gaacttggaa ggcctgcac atgatggcca attctgccat aagccctgtc ctccagggtga 420
aaggaaagct agggactgca cagtcaatgg ggatgaacca gactgcgtgc cctgccaaga 480
agggaaaggag tacacagaca aagccattt ttcttccaaa tgcagaagat gtagattgtg 540
tgatgaagga catggccttag aagtggaaat aaactgcacc cggaccaga ataccaagt 600
cagatgtaaa ccaaactttt ttgttaactc tactgtatgt gaacactgtg acccttgca 660
caaatgtgaa catggaatca tcaaggaatg cacactcacc agcaacac ca agtgcaaaaga 720
ggaaggatcc agatctaact tgggttggct ttgtcttctt cttttgcca ttccactaat 780
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cagaaatgaa atccaaagct tggctctagag tgaaaaacaa caaattcagt tctgagtata 1260
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acagtttatt ggtgtcatat tatacaatat ttcaattgtg aattcacata gaaaacatta 1860
aattataatg ttgactatt atatatgtgt atgcatttta ctggctcaaa actacctact 1920
tctttctcag gcatcaaaag cattttgagc aggagagtat tactagagct ttgccacctc 1980
```

98/292

```

tccatttttg ccttggtgct catcttaat g gcctaattgca cccccaaaca tggaaatata 2040
accaaaaaat acttaatagt ccaccaaag gcaagactgc ccttagaaat tctagcctgg 2100
tttgagata ctaactgctc tcagagaaag tagctttgtg acatgtcatg aacccatgtt 2160
tgcaatcaaa gatgataaaa tagattctta tttttccccc acccccgaaa atgttcaata 2220
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ggaaccacct aaagaacttc catttatgga ggattttttt gccccttggtg ttggaatta 2520
taaaatatag gtaaaagtac gtaattaaat a 2551

```

<210> 144

<211> 434

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(434)

<223> 3' terminal sequence. cyclin -dependent
kinase inhibitor 1a (p21, cip1) (CDKN1A) gene.

<400> 144

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aaagtcacta agaatcattt attnagcacc tgctgtatat tcagcattgt gggaggagct 60
gtgaaagaca cagaacagta cagggtgtgg tccctgccct cgagagggtt acagtctagg 120
tgagagaaac ggaaccagga cacatgggga gccgagagaa aacagtccag gccagtatgt 180
tacaggagct ggaaggtntt tggggtcaga cccaatact ccaagtacac taagcatttc 240
agtccttcca ggggtcgaac gttagtcca ggaagacaa ctactcccag ccccatatga 300
gccacgtgg catgccctgt ccatagcctc tactgccacc atcttaaaat gtctgactcc 360
ttgttcgct ggctaattca aagtgcaatg aactggggag ggatggggtg gatgaggaag 420
gttcgntgga cgtt 434

```

<210> 145

<211> 257

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(257)

<223> 5' terminal sequence. cyclin -dependent
kinase inhibitor 1a (p21, cip1) (CDKN1A) gene.

<400> 145

```

cttgtgtgct ntncagggg a gcaggctgaa ggggtccccag gtggacctgg agactctcag 60
ggtcgaaaac ggcgagagac cagcatgaca gatttctacc actccaaacg ccggctgac 120
ttctccaaga ggaagcccta atccgcccac aggaagcctg cagtcttgga agcgagagg 180
cctcaaaggc cntnctnaca tcttctgcct tagtctcagt ttgtgtgtct taattattat 2 40
ttgtgtttta aattttt 257

```

<210> 146

<211> 2121

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2121)

<223> cyclin-dependent kinase inhibitor 1a (p21,
cip1) (CDKN1A) gene.

<400> 146

```
gccgaagtca gttccttggt gagccggagc tgggcgcgga ttgcgcgagg caccgaggca 60
ctcagaggag ggcgcatgtc agaaccggct ggggatgtcc gtcagaaccc atgcggcagc 120
aaggcctgcc gccgcctctt cggcccagtg gacagcgagc agctg agccg cgactgtgat 180
gcgctaattg cgggctgcat ccaggaggcc cgtgagcgat ggaacttcga ctttgtcacc 240
gagacaccac tggagggtga cttegcctgg gagcgtgtgc ggggccttgg cctgcccagg 300
ctctaccttc ccacggggcc ccggcgaggc cgggatgagt tgggaggagg caggcggcct 360
ggcacctcac ctgctctgct gca ggggaca gcagaggaa accatgtgga cctgtcactg 420
tcttgtaccc ttgtgcctcg ctacggggag caggctgaag ggtccccagg tggacctgga 480
gactctcagg gtcgaaaacg gcggcagacc agcatgacag atttctacca ctccaaacgc 540
cggtgatctt tctccaaagag gaagccctaa tccgcccaca ggaagcctgc agtcctggaa 600
gcgcgagggc ctcaaaggcc cgctctacat cttctgcctt agtctcagtt tgtgtgtctt 660
aattattatt tgtgttttaa tttaaacacc tctcatgta catacctgg ccgccccctg 720
ccccccagcc tctggcatta gaattattta aacaaaaact aggcggttga atgagagggt 780
cctaagagtg ctgggcattt ttattttatg aaatactatt taa agcctcc tcatcccggt 840
ttctcctttt cctctctccc ggaggttggg tgggcgggct tcatgccagc tacttccctc 900
tccccacttg tccgctgggt ggtaccctct ggaggggtgt ggctccttcc catcgctgtc 960
acaggcgggt atgaaattca ccccccttcc tggacactca gacctgaatt ctttttcatt 1020
tgagaagtaa acagatggca ctttgaaggg gcctcaccca gtgggggcat catcaaaaac 1080
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ggcaggggga aggtggggta ctggagcaga ccaccccgcc tgccctcatg gccctctga 1260
cctgcactgg ggagcccgtc tcagtgttga gccttttccc tctttggctc cctgtacct 1320
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cctgtcccac cccaccccc agtcaatgg actg gaaggg gaagggacac acaagaagaa 1500
gggcacccca gttctacctc aggcagctca agcagcgacc gccccctcct ctagctgtgg 1560
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gctcatatgg ggctgggagt agttgtcttt cctggcacta acgttgagcc cctggaggca 1860
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taacatactg gcctggactg tttctctctg gctccccatg tgtcctgggt cccgtttctc 1980
cacctagact gtaaacctct cgagggcagg gaccacaccc tgtactgttc tgtgtctttc 2040
acagctcctc ccacaatgct gaataacag cagggtgtca ataaatgatt cttagtgact 2100
ttaaaaaaaa aaaaaaaaaa a
```

2121

<210> 147

<211> 452

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(452)

<223> 3' terminal sequence. phospholipase a2,
group iia (platelets, synovial fluid) (PLA2G2A)
gene.

<400> 147

```
gatttgctaa ttgctttatt cagaagagac ccccgaggat acagcttctt tggtaagca 60
cggagttgag gtggaggaga gcagtagaag gctggaaatc tgctggatgt ctcattctgg 120
gtgggtatag aagggtcctt gcctggcctc taggatgggt gagggatgct ttctgcatgg 180
ccaaggaact tggtaggggt agggagggag ggtatgagag agggaaattc agcactgggt 240
ggaaggtttc caggaagag gggactcagc aacgaggggt gctccctctg cagtntttat 300
tggaatagta ctggtacttt ttattgtagg tcgtcttntt tctagcaaaa cagggtngca 360
gcagccttat cacacttca c acagttgact tctgcaggag tccnttttt gcacaggttg 420
attctgctoc ccgaagttac taaacttttt tt 452
```

<210> 148

<211> 379

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(379)

<223> 5' terminal sequence. phospholipase a2,
group iia (platelets, synovial fluid) (PLA2G2A)
gene.

<400> 148

```
tggagtcctc tgagagagcc accaaggagg agcaggggag cgacggccgg ggcagaagtt 60
gagaccaccc agcagaggag ctaggccagt ccatctgc at ttgtcaccca agaactotta 120
ccatgaagac cctcctactg ttggcagtga tcatgatctt tggcctactg caggcccatg 180
ggaatttgggt gaatttccac agaatgatca agttgacgac aggaaggaa gccgcactca 240
gttatggctt ctacggctgc cactgtggcg tgggttgagc aggatcccc aaggatgcaa 300
cggattcgct gctgtgtcac tcatgactgt ttgctacaaa cgtctgggag aaacgtgggt 360
tnttggcacc aaatttttt 379
```

<210> 149

<211> 854

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(854)

<223> phospholipase a2, group iia (platelets,
synovial fluid) (PLA2G2A) gene.

<400> 149

```
gaattcccaa ctctggagtc ctctgagaga gccaccaagg aggagcaggg gagcgacggc 60
cggggcagaa gttgagacca cccagcagag gagctaggcc agtccatctg catttgtc ac 120
ccaagaactc ttaccatgaa gaccctccta ctgttggcag tgatcatgat ctttggccta 180
ctgcaggccc atgggaattt ggtgaatttc cacagaatga tcaagttgac gacaggaaag 240
gaagccgcac tcagttatgg cttctacggc tgccactgtg gcgtgggtgg cagaggatcc 300
```

cccaaggatg caacggatcg ctgctgtgtc actcat gact gttgctacaa acgtctggag 360
aaacgtggat gtggcaccaa atttctgagc tacaagttaa gcaactcggg gagcagaatc 420
acctgtgcaa aacaggactc ctgcagaagt caactgtgtg agtgtgataa ggctgctgcc 480
acctgttttg ctagaaacaa gacgacctac aataaaaagt accagtacta ttccaataaa 540
cactgcagag ggag cacccc tcgttctga gtccctctt ccctggaaac ctccaccca 600
gtgctgaatt tccctctctc ataccctccc tccctaccct aaccaagttc cttggccatg 660
cagaaagcat ccctcaccca tcctagaggc caggcaggag cccttctata cccaccaga 720
atgagacatc cagcagattt ccagccttct actgctctcc tccacctcaa ctccgt gctt 780
aaccaaagaa gctgtactcc ggggggtctc ttctgaataa agcaattagc aaatcaaaaa 840
aaaaaaagga attc 854

<210> 150

<211> 224

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:p rimer

<220>

<221> misc_feature

<222> (1)..(224)

<223> 3' terminal sequence.

glyceraldehyde-3-phosphate dehydrogenase (GAPD)
gene.

<400> 150

ggttgagcac agggactttt attgatggna catgacaagg tgcggctccc taggcccctc 60
ccctnttcaa ggggtctaca tggcaact nt gaggagggga gattcagtgt ggtgggggac 120
tgagtntggc agggactccc cagcagttag ggtctctctc ttcctcttnt gctcttncgt 180
gggntgggtg nccagggntn ttactccttg gaggccatnt gggc 224

<210> 151

<211> 359

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(359)

<223> 5' terminal sequence.

glyceraldehyde-3-phosphate dehydrogenase (GAPD)
gene.

<400> 151

gcgctgagta cgtcgtggag tccactggcg tcttcaccac catggagaag gctgggggctc 60
atttgcaggg gggagccaaa agggatcatca tctctgcccc ctctgctgat gcccccatgt 120
tcgtcatggg tgtgaacctat gagaagtatg acaacagcct caagatcatc agcaatgcct 180
cctgcaccac caactgctta gcacccttg gccaaagtca tccatgacaa ctttggatc 240
gtggaaggac tcatgaccac agtccatgcc atcactgcca c ccagaagac tgtggatggc 300
ccctncggga aactgtgggc gtgatggccg cggggttctt tcagaacatc atccctgcc 359

<210> 152

<211> 1283

<212> DNA/RNA

102/292

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1283)

<223> glyceraldehyde -3-phosphate dehydrogenase
(GAPD) gene.

<400> 152

```
ctctctgctc ctctgttgc acagtcagcc gcatcttctt ttgcgtcgcc agccgagcca 60
catcgctcag acaccatggg gaaggtgaag gtcggagtca acggatttgg tcgtattggg 120
cgccctggta ccagggtctc tttaactct ggta aagtgg atattgttgc catcaatgac 180
cccttcattg acctcaacta catggtttac atgttccaat atgattccac ccatggcaaa 240
ttccatggca cgtcaaggc tgagaacggg aagcttgtca tcaatgaaa tcccatcacc 300
atcttccagg agcgagatcc ctccaaaatc aagtggggcg atgctggcgc tgagtacgtc 360
gtggagtcca ctggcgtctt caccaccatg gagaaggctg gggctcattt gcagggggga 420
gccaaaaggg tcatcatctc tgccccctct gctgatgccc ccatgttcgt catgggtgtg 480
aaccatgaga agtatgacaa cagcctcaag atcatcagca atgcctcctg caccaccaac 540
tgcttagcac ccctggccaa ggtcatccat gacaactttg gtatcgtgga agga ctcatg 600
accacagtc atgccatcac tgccaccag aagactgtgg atggccctc cgggaaactg 660
tggcgtgatg gccgcggggc tctccagaac atcatccctg cctctactgg cgctgccaag 720
gctgtgggca aggtcatccc tgagctgaac gggaagctca ctggcatggc cttccgtgtc 780
cccactgcca acgtgtcagt ggtggacctg ac ctgccgtc tagaaaaacc tgccaaatat 840
gatgacatca agaaggtggg gaagcaggcg tcggagggcc ccctcaaggg catcctgggc 900
tacatgagc accaggtggg ctctctgac ttcaacagcg acaccactc ctccacctt 960
gacgttgggg ctggcattgc cctcaacgac cactttgtca agctcatttc ctggtatgac 1020
aacgaatttg gctacagcaa cagggtgggtg gacctcatg ccacatggc ctccaaggag 1080
taagaccctt ggaccaccag cccagcaag agcacaagag gaagagagag accctcactg 1140
ctggggagtc cctgccacac tcagtcccc accacactga atctccctc ctacagtgtg 1200
ccatgtagac ccctgaaga ggggaggggc ctaggagacc gcacctgt c atgtaccatc 1260
aataaagtac cctgtgctca acc                                     1283
```

<210> 153

<211> 361

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(361)

<223> 3' terminal sequence. jun b proto -oncogene
(JUNB) gene.

<400> 153

```
tacttaata gattcaatan aaagaacaaa cacacacaaa cacaacacg tcttaaaata 60
aactctttag agactaagtg cgtgttctt ttccacagta cgggtgcagag aggggagggc 120
agggggcggg ggtcccttcc caatgtcccc gcgggcttga gta ccaggcg gcggggccag 180
ctcccontant ncgccccctc ttccctccc tgtaaatac acaaataat tatattcaat 240
ntgaatcgng tctntttcca gcagaaaaaa aacatacaaa aaaaagtggg aagggggggg 300
cttntttaa cgttcggang ttggaaggnc tttggggcnc aggggtaggg anggcccgag 360
t                                     361
```

<210> 154

<211> 401
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(401)
<223> 5' terminal sequence. jun b proto -oncogene
(JUNB) gene.

<400> 154
agcgcatcaa agtngagcgc angccttgcg gaaccggctn gcggccacca agtgccggaa 60
gcggaantgg gagcgcatcg ggcttgggag gacaagggtga agacgctcaa ggccgagaac 120
gcggggntgt cgagtaccgc cggcttcctc cgggagcagg tggcccagct caaacagaag 180
gtcatgaccc acgtnagc aa cggctntnag ctgctgcttn gggtaaggga acacgccttc 240
tggaacgttc cctgccccctt tacgggacac ccccttcgtt tnggacggtt nggcacacgg 300
tttcccactn ggggttcagg gtagcaggcg gtgggnacc cactggggg acntaggggg 360
cgncgcgaaa ccacattngg atttccggcc ttcttaacct t 401

<210> 155
<211> 1797
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1797)
<223> jun b proto -oncogene (JUNB) gene.

<400> 155
ccagcaggga gctgggagct gggggaaacg acgc caggaa agctatcgcg ccagagaggg 60
cgacgggggc tcgggaagcc tgacagggtt ttgcgacaca gctgccggct ggctgctacc 120
gcgccgcgbc agccccgag aacgcgcgac caggcaccca gtccgggtcac cgcagcggag 180
agctcgccgc tcgctgcagc gaggcccgga gcggccccgc agggaccctc ccagaccgc 240
ctgggcccgc cggatgtgca ctaaaatgga acagcccttc taccacgacg actcatacac 300
agctacggga tacggccggg cccctggtgg cctctctcta cagactaca aactcctgaa 360
accgagcctg gcggtcaacc tggccgaccc ctaccggagt ctcaaagcgc ctggggctcg 420
cggaccgggc ccagagggcg gcggtggcg cagctacttt tctggtcagg gctcg gacac 480
cggcgcgctc ctcaagctcg cctcttcgga gctggaacgc ctgattgtcc ccaacagcaa 540
cggcggtgat acgacgacgc ctacaccccc gggacagtac ttttaccccc gcgggggtgg 600
cagcgggtga ggtgcagggg gcgcaggggg cggcgtcacc gaggagcagg agggcttcgc 660
cgacggcttt gtcaaagccc tggacgatct gca caagatg aaccacgtga cccccccaa 720
cgtgtccctg ggcgtaccg gggggcccc ggctgggccc gggggcgtct acgccggccc 780
ggagccacct cccgtttaca ccaacctcag cagctactcc ccagcctctg cgtcctcggg 840
aggcgccggg gctgccgtcg ggaccgggag ctcgtaaccg acgaccacca tcagctacct 900
cccacacgcg ccgcccctcg ccggtggcca cccggcgag ctgggcttgg gccgcggcgc 960
ctccaccttc aaggaggaac cgcagaccgt gccggaggcg cgcagccggg acgccacgcc 1020
gccggtgtcc cccatcaaca tggaagacca agagcgcatc aaagtggagc gcaagcggct 1080
gcggaaccgg ctggcgccca ccaagtgcg gaagcggaag ctggagcgca t cgcgcgct 1140
ggaggacaag gtgaagacgc tcaaggccga gaacggggg ctgtcgagta ccgccggcct 1200
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acccctcgc ttggacggct gggcac acgc ctcccactgg ggtccaggga gcaggcgggtg 1380
ggcaccacac ctgggacctt gggcgccgc aaaccacact ggactccggc cccctaccc 1440

104/292

tgcgcccagt ccttccacct cgacgtttac aagccccccc ttccactttt ttttgtatgt 1500
tttttttctg ctggaaacag actcgattca tattgaatat aatataattg tgtatttaac 1560
agggagggga agagggggcg atcgcgcgag agctggcccc gccgcctggt actcaagccc 1620
gcggggacat tgggaaggag acccccgccc cctgccttcc cctctctgca cgtactgtg 1680
gaaaagaaac acgcacttag tctctaaaga gtttatttta agacgtgttt gtgtttgtgt 1740
gtgtttgttc tttttattga atctatttaa gtaaaaaaaa aattggttct ttattaa 1797

<210> 156

<211> 335

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(335)

<223> 3' terminal sequence. cellular retinoic
acid-binding protein 2 (CRABP2) gene.

<400> 156

aagcatttta ataaaattaa caaataaata ttctaaactg tataggctac agggacaaaag 60
ggtagaagct agagggccag tcttctctgc tcaggccctc aagtcctctt tagagagacc 120
ctgctctggg ctggtttggg gctaggactg ctgacttggg gaggcgggga gtgaacccgg 180
aatgggtgat ctgggctctt gcagccattc ctctttgttg gtgtagggga ggagagaaga 240
ggtaaaagaa agcaagaccg tgcaagaggc atcccagtga cccccagaag tgactggggg 300
aaggggagcg ctatcctagg anggtggggg tgggt 335

<210> 157

<211> 481

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(481)

<223> 5' terminal sequence. cellular retinoic
acid-binding protein 2 (CRABP2) gene.

<400> 157

gcctggactt gtcttggggt ccagaacctg acgaccggc gacgcgacgt ctct ttgac 60
taaaagacag tgtccagtgc tccagcctag gagtctacgg ggaccgcctc ccgcgccgcc 120
accatgccca acttctctgg caactggaaa atcatccgat cggaaaactt cgaggaattg 180
ctcaaagtgc tnggggtgaa tgtgatgctg aggaagattg ctgtggctnc agcgtccaag 240
ccagcagtng agatcaaaca ggaggagac act ttctaca tcaaaacctc caccaccgtg 300
cggcaccaca gagattaact tcaagggtng ggaggagttt gagggagcag antgtgggtg 360
gggaggccct gttaaggagc ngggtgaaat ggggagagtg aggattaaat ggtcttttga 420
gcagaagttc ctgaaggng aggggccccca agaentcttg gaccngagaa tttncaccag 480
t 481

<210> 158

<211> 969

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(969)

<223> cellular retinoic acid -binding protein 2
(CRABP2) gene.

<400> 158

```
agctttgggg ttgtccctgg acttgtcttg gttccagaac ctgacgaccc ggcgacggcg 60
acgtctcttt tgactaaaag acagtgtcca gtgctccagc ctaggagtct acgggggaccg 120
cctcccgcgc cgccaccatg cccaacttct ctggcaactg gaaaatcatc cgatcggaag 180
acttcgagga attgctcaaa gtgctggggg tgaatgtgat gctgaggaag attgctgttg 240
ctgcagcgtc caagccagca gtggagatca aacaggaggg agacactttc tacatcaaaa 300
cctccaccac cgtgcgcacc acagagatta acttcaaggt tggggaggag tttgaggagc 360
agactgtgga tgggaggccc tgtaagagcc tggtagaatg ggagag tgag aataaaatgg 420
tctgtgagca gaagctcctg aaggagaggg gcccgaagac ctctgtggacc agagaactga 480
ccaacgatgg ggaactgatc ctgaccatga cggcggatga cgttgtgtgc accagggtct 540
acgtccgaga gtgagtggcc acaggtagaa ccgcggccga agcccaccac tggccatgct 600
caccgccttg cttcactgcc ccct ccgtcc caccctcc ttctaggata gcgctccct 660
taccacagtc acttctgggg gtcactggga tgctcttgc aggtcttgc tttctttgac 720
ctcttctctc ctcccctaca ccaacaaga ggaatggctg caagagccca gatcacccat 780
tcggggttca ctcccgcct cccaagtca gcagtcctag ccccaaacca gccagagca 840
gggtctctct aaaggggact tgagggcctg agcaggaaag actggccctc tagcttctac 900
cctttgtccc tgtagcctat acagtttaga atatttattt gttaatttta ttaaatgct 960
ttaaaaaaa                                     969
```

<210> 159

<211> 344

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(344)

<223> 3' terminal sequence. activin a receptor
type ii-like 1 (ACVRL1) gene.

<400> 159

```
cgcgnttggg ggggaggttg ccccgntcc gccgangaan tcgccccg cc accgcagag 60
cncncagagg gaccattgac cttgggctcc ccaggaag gccttctgat gctgctgatg 120
gccttggtga ccaggggaga cctgtgaag ccgtctcggg gccgctggt gacctgcacg 180
tgtgagagcc cacattgcaa ggggcctacc tgccgggggg cctgggtgca cagtagtgct 240
tggtgcggg aggaggggag gcacccc cag ggaacattcg gggntgcggg aantttgcac 300
agggagntct tgacgggggg gcgccccacc gatttcgttc aacc                                     344
```

<210> 160

<211> 416

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(416)
<223> 5' terminal sequence. activin a receptor
type ii-like 1 (ACVRL1) gene.

<400> 160
gtcagtctcc cggaaccagg actgttcac cctcgaggag aagatcttga cggccacact 60
ctcaccgtgc cacaagcccc gccacacttc gccatagcgc cttttccac acactccacc 120
aaggcaacct gccgtngcca ctgtcctctg caccaggga ggggagccct gagccactcc 180
ctgtgggtgg cagtactgt ccaggagggt ccccaacat gctgttcgcc ctgcttcaga 240
tgcttttcag ggatgaggat gggattttcc cagcttcgct gttgcagggc cagttgctt 300
tttccttgcc tncgttcggg acatggccac agggcccagg ggacaaccag g gggccacca 360
gggggnccag gcaanggcca agnacgggg ggcccagggt ttnaagggc cagttt 416

<210> 161
<211> 1970
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1970)
<223> activin a receptor type ii-like 1 (ACVRL1)
gene.

<400> 161
aggaaacggt ttattaggag ggagtgggtg agctgggcca ggcaggaaga cgctggaata 60
agaaacattt ttgtccagc ccccatccca gtcccgggag gctgccgcgc cagctgcgcc 120
gagcgagccc ctcccgggt ccagccgggt ccggggccgc gccggaccc c agcccgcgt 180
ccagcgctgg cggtgcaact gcggccgcgc ggtggagggg aggtggcccc ggtccgccga 240
aggctagcgc cccgccacce gcagagcggg ccagaggga ccatgacctt gggtccccc 300
aggaaaggcc ttctgatgct gctgatggcc ttggtgacct agggagacct tgtgaagccg 360
tctcggggcc cgctggtgac ctgcacg tgt gagagccac attgcaaggg gcctacctgc 420
cggggggcct ggtgcacagt agtctggtg cgggaggagg ggaggcaccc ccaggaaacat 480
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caacctcctt cggagcagcc gggaacagat ggccagctgg cctgatcct gggccccgtg 660
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caggagaagc agcgtggcct gcacagcgag ctgggagagt ccagtctcat cctgaaagca 780
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aaccgcagag tgggcaccaa gcggcagag tgctggacga gcagatccgc 1440
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atgatcgagg agtgctggt cccaaacccc tctgcccagc tcaccgcgct gcggatcaag 1740
aagacactac aaaaaattag caacagtcca gagaagccta aagtgattca atagcccagg 1800

107/292

agcacctgat tcctttctgc ctgcaggggg ctgggggggt ggggggcagt ggatggtgcc 1860
ctatctgggt agaggtagt tgagtgtgt gtgtgctgg gatgggcagc t gcgcctgcc 1920
tgctcggccc ccagcccacc cagccaaaaa tacagctggg ctgaaacctg 1970

<210> 162

<211> 407

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(407)

<223> 5' terminal sequence. lim domain protein
(RIL) gene.

<400> 162

gtgacctgc gggggccttc gccctggggc ttccgcctgg tngggccgng gacttcagcg 60
cgccccctac catctcacgg gtccatgctg gcagcaaggc tcatntggct gccctgtgcc 120
caggagacct gatccaggcc atcaatggtg agagcacaga gctcatgac a cacctggang 180
cacagaaccg catcaagggc tgccacgata acctcacact gtctgtgagc aggcctgagg 240
gcaggagctg gccagtgcc cctgatgaca gcaaggctca ggcacacagg atccacatcg 300
ntcctgagat ccaggacggc agccaacaa ccagcaggcg gccctcaggc accgggactt 360
gggccagaag atnnggcagan caagnct ggg gtttttncat atggaca 407

<210> 163

<211> 1130

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1130)

<223> lim domain protein (RIL) gene.

<400> 163

tgagagtccg gctcaggctc cggtgcggc tccagccgc gatgcccac tccgtgacct 60
tgcgcgggcc ttgcacctgg ggcttcggcc tgggtgggccc ggacttcagc gcgccccctca 120
ccatctcacg ggtccatgct ggcagcaagg cctcattggc tgccctgtgc ccaggagacc 180
tgatccaggc catcaatggt gagagcacag agctcatgac acacctg gag gcacagaacc 240
gcatcaaggc ctgccacgat cacctcacac tgtctgtgag caggcctgag ggcaggagct 300
ggccccagtc ccctgatgac agcaaggctc aggcacacag gatccacatc gatcctgaga 360
tccaggacgg cagcccaaca accagcaggc ggccctcagg caccgggact gggccagaag 420
atggcagacc aagcctggga tctcc atatg gaaaaccccc ttgctttcca gtccctcaca 480
atggcagcag cgaggccacc ctgccagccc agatgagcac cctgcatgtg tctccacccc 540
ccagcgtga cccagcagag gcctcccgcg gagccgggag cagagtcgac ctgggctccg 600
aggtgtacag gatgctgcgg gagccggccg agcccgtggc cgcggagccc aagcagtcag 660
gctccttccg ctacttgacg ggcatgctag aggcgggcca gggcggggat tggcccgggc 720
ctggcgggcc ccggaacctc aagcccacgg ccagcaagct gggcgctccg ctgagcggcc 780
tgcaagggtc gcccgagtgc acgcgtgct gccacggaat cgtgggcacc atcgtcaagg 840
aacgggacaa gctctacat cccgagtgtc tcatgtgcag tgact gcggc ctgaacctca 900
agcagcgtgg ttacttcttt ctggacgagc ggctctactg tgagagccac gccaaaggcg 960
gcgtgaagcc gcccgagggc tacgacgtgg tggcggtgta cccaatgcc aaggtggaac 1020
tcgtctgagc tgggacctg ctcccacccc tgcttcttaa ggtccctgct cggccgggtg 1080

108/292

aaatatgttt caccctgtcc c tctaataaa gtcctctctgc tcaaaaaaaaa

1130

<210> 164

<211> 310

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(310)

<223> 5' terminal sequence. shc (src homology 2 domain-containing) transforming protein 1 (SHC1) gene.

<400> 164

anattcggaa cgagggatcc ctcttatgtc aacgtccaga acctagacaa ggcccggcaa 60
gcagtgggtg gtgctggggc ccccaatcct gctatcaatg gcagtgcacc ccgggacctg 120
tttgacatga agcccttcga agatgctctt cgcgtgc ctc cacctcccca gtcggtgtcc 180
atgntcagc agctccgagg ggagccctgg gttccatggg aagctgagcc ggcgggaggc 240
tgaggcactg ctggcagctt caatggggat ttccnggtac gggagagcac gaccacacng 300
gggcaatatg 310

<210> 165

<211> 3664

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3664)

<223> shc (src homology 2 domain -containing) transforming protein 1 (SHC1) gene.

<400> 165

atggggcctg aaactgtctg ggtctgagct ggggagcgga agccacttgt ccctctccct 60
ccccaggact tctgtgactc ctgggccaca gagggtccaac cagggttaagg gcctggggat 120
accccttgcc tggcccccctt gcccaaaactg gcaggggggc caggctgggc agcagcccct 180
ctttcacctc aactatggat ctctgcccc ccaagcccaa gtacaatcca ct ccggaatg 240
agtctctgtc atcgctggag gaaggggctt ctgggtccac cccccggag gagctgcctt 300
ccccatcagc ttcattccctg gggcccatcc tgccctcctct gcctggggac gatagtccca 360
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ggcgcccagg gtctaagggg gagccaggaa gggcagctga tgatggggag gggatcgatg 480
gggcagccat gccagagtca ggccccctac ccctcctcca ggacatgaac aagctgagtg 540
gaggcgccgg gcgcaggact cgggtggaag ggggccagct tgggggcgag gagtggaccc 600
gccacgggag ctttgtcaat aagcccacgc ggggctggct gcatcccaac gacaaagtea 660
tgggaccggg ggtttcctac ttggttcggg acatgggttg tgtggaggtc ctccagtcaa 720
tgcgtgcctt ggacttcaac acccggaact aggtcaccag ggaggccatc agtctggtgt 780
gtgaggctgt gccgggtgct aagggggcga caaggaggag aaagccctgt agccgcccgc 840
tcagctctat cctggggagg agtaacctga aatttgctgg aatgccaatc actctcaccg 900
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ttgcccagga tgcacatcag accattg gcc aggccttcga gttgcgcttc aaacaatacc 1140

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cccggcaagc agtgggtggt gctgggcccc ccaatcctgc tatcaatggc agtgcacccc 1560
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tggacctga gggtgtggtt cggactaagg atcaccgctt tgaaagtgtc agtcacctta 1860
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actctccag gtggatt ttgagggtgag aaaaggggca ttgagactat aaagcagtag 2880
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ggcctgtgag gtaactggga tcgcaccttt tataccagag acctgaggca gatgaaattt 3600
atttccatct aggactagaa aaacttgggt ctcttaccgc gagactgaga ggcagaagtc 3660
agcc
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3664

<210> 166

<211> 449

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(449)

<223> 3' terminal sequence.

glyceraldehyde-3-phosphate dehydrogenase (GAPD)
gene.

<400> 166

110/292

```
gagcacaggg tncctttattg atggtacatg acaagggtgcg gctccctagg cccctcccct 60
cttcaagggg tctacatgga aactgtgagg aggggagatt cagtgtggtg ggggactgag 120
tntggcaggg actccccagc agtgagggtc tctctcttcc tcttgtgctc ttgctggggc 180
tggtggtcca ggggtcttac tccttgaggg ccatgtgggc atgagggtcca ccacctgtt 240
gctgtagcca aattcgttgt cataccaggg aaatgagctt gacaaagtgg tcgttgaggg 300
caatgccagc cccagccttc gaagggtggag gantggggtt cgctnttgaa gtcagaggag 360
accacctggg tgctcagttt agcccagggg tgcccttgag ggggccctcc gacgttt ttt 420
tcaccacctt tttgatntca tcatntttt 449
```

<210> 167

<211> 467

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(467)

<223> 5' terminal sequence.

glyceraldehyde-3-phosphate dehydrogenase (GAPD)
gene.

<400> 167

```
tggttcgacag tcagccgcat cttcttttgc gtcgccagcc gagccacatc gctgagacac 60
catggggaag gtgaaggtag gagtcaacgg atttggtcgt attgggcgcc tggtcaccag 120
ggctgctttt aactctggta aagtggata t tgttgccatc aatgaccctc tcattgacct 180
caactacatg gtttacatgt tccaatatga ttccacccat gggcaaattc catgggcacc 240
gtcaaggctg agaacgggaa gcttgtcatc aatgggaaat cccattcacc atcttccagg 300
gagcgagatc cctccaaaat tcaagtgggg ggcgatgctg ggcgcttgag ttacgttcgt 360
gggagttcca ctgggccttc tttcaaccac ccttgagaga gggtttgggg gttcattttt 420
caaggggggg gagcccaaan ggtcttcat tttttggccc ccttttt 467
```

<210> 168

<211> 316

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(316)

<223> 3' terminal sequence. desmin (DES) gene.

<400> 168

```
ggcttgtgtt tnttntctct ttattgtttc tctccagagc ccctgcagca ggggagggga 60
gggcgtgggg aggtgggcgc ccctcccacc agcctgagac cgctctctgc ctctctctc 120
tctctcttc tccagcatct cac ccacttt ctctccttct naatctcctg ctcccacctc 180
cagcaccttc ggggattccc tctttagacc cctgctttct aagtccaccc ggggctgggg 240
aaaggaaagt aagagaccac ggggacaatt tcaagcccc cagtntccac aggggctagt 300
ccctgggnt acctgc 316
```

<210> 169

<211> 440

<212> DNA

111/292

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(440)

<223> 5' terminal sequence. desmin (DES) gene.

<400> 169

```
atctcccat ccagacctac tctgccctca acttccgag a aaccagccct gagcaaagg 60
gttctgaggt ccataccaag aagacggtga tgatcaagac catcgagaca cgggatggg 120
aggtcgtcag tgaggccaca cagcagcagc atgaagtgt ctaaagacag agaccctctg 180
ccaccagaga ccgtcctcac ccctgtcctc actgctcct gaagccagcc ttcttccatc 240
ccagggacac cacaccca gc cttcagtcct ccccttcaca gcctctggac ccctcctcac 300
tgggccattc cctcgtggtt ccccaacagc ggacataggc ccaccttgc tgggttcaca 360
ggggcatggc cccgggccac ttnttgcggg aaccacagtt gttgaggctt tgggtgtttg 420
ggcagttgag ttgaggcttt
```

440

<210> 170

<211> 2218

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2218)

<223> desmin (DES) gene.

<400> 170

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gcctcgcccg cgccgtcacc atgagccagg cctactcgtc cagccagcgc gtgtcctcct 120
accgcccgcac cttcggcggc gcccggggt tcccgctcgg ctccccgctg agctcgcccg 180
tggtcccgcg ggccgggttc ggctctaagg gctcctccag ctcggtgacg tcccgctgtg 240
accaggtgtc ggcacgtcg ggccggg ccg ggggcctggg gtcgctggcg gccagccggc 300
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ccgacgcggt gaaccaggag ttctgacca cgcgcaccaa cgagaagggt gagctgcagg 420
agctcaatga ccgttcgcc aactacatcg agaagggtgcg ctctcctggag cagcagaacg 480
cgctcgccgc cgaagtgaac cggctcaagg gccgcgagcc gacgcgagtg gccgagctct 540
acgaggagga gctgcgggag ctgcggcgcc aggtggaggt gctcactaac cagcgcgcg 600
gcgtcgacgt cgagcgcgac aacctgctcg acgacctgca gcggctcaag gccaaagctgc 660
aggaggagat tcagttgaag gaagaagcag agaacaattt ggctgcc ttc cgagcggacg 720
tggatgcagc tactctagct cgcattgacc tggagcgag aattgaatct ctcaacgagg 780
agatcgcggt ccttaagaaa gtgcatgaag aggagatccg tgagttgcag gctcagcttc 840
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atggggaggc cgtcagtgag gcgacacagc agcagcatga agtgctctaa agacgagaga 1500
ccctctgcca ccagagaccg tcctcaccct tgtcctcact gctccctgaa gcccagcctt 1560
```


112/292

```

cttccatccc agga caccac acccagcctc agtctctccg tcacagcctc tgaccctcc 1620
tcaactggcca tccctcgtgg tcccaacag cgacatagcc catccctgcc tggtcacagg 1680
catgcccccg ccacctctgc ggacccacg tgtgagcctt ggtgttggtc agtgagttag 1740
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tgctggagaa gagagaggag gagagaggca gagagcggtc tgaggctggt gggaggggag 2160
cccacctccc cagccctccc cccccctgc tgcaggggct ctggagagaa acaataaa 2218

```

<210> 171

<211> 367

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(367)

<223> 5' terminal sequence. casein kinase 2, beta polypeptide (CSNK2B) gene.

<400> 171

```

gatccacgcc cgctacatcc ttaccaaccg tggcatcgcc agatgttggg aaagtaccag 60
caaggagact ttggttactg tctcgtgtg tactgtgaga accagccaat gcttcccatt 120
ggcctttcag acatcccagg tgaagccatg gtgaagctct actgccccaa gtgcatggat 180
gtgtacacac ccaagtcacg aagacacccat cacacggatg ggcgcctac t ttcggcactg 240
gtttccctca catgctcttc atgggtgcat cccgagtacc ggcccaaggg gaccttgcca 300
accagtttgt gccaggggtt ttacggtttt caaggttcca tncgggtggg cttaccaggt 360
tgcaggt 367

```

<210> 172

<211> 1128

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1128)

<223> casein kinase 2, beta polypeptide (CSNK2B) gene.

<400> 172

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tgccggggtc atcctgggat tggtagttcg ctttctctca tttagccagt ttctttctct 120
accggggact ccgtgtcccg gcattccacc cggcaacctga cccttggcgc ttgctgtgtg 180
cctctttccc caccctccct aatttccact cccccaccc cacttcgcct gccgcggtcg 240
ggtccgcggc ctgctgtgta gcgg tcgccc ccgttccctg gaagtagcaa cttccctacc 300
ccacccagct cctggtcccc gtccagccgc tgacgtgaag atgagcagct cagaggaggt 360
gtcctggatt tctgtgtct gtgggtccg tggcaatgaa ttcttctgtg aagtggatga 420
agactacac caggacaaat ttaatcttac tggactcaat gagcaggctc ctcactatcg 480
acaagctcta gacatgatct tggacctgga gcctgatgaa gaactggaag acaaccccaa 540

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113/292

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ccagagtgc ctgattgagc aggcagccga gatgctttat ggattgatcc acgcccgcta 600
catccttacc aaccgtggca tgcgccagat gttggaaaag taccagcaag gagactttgg 660
ttactgtcct cgtgtgtact gtgagaacca gccaatgctt ccca ttggcc ttccagacat 720
cccagggtgaa gccatggtga agctctactg ccccaagtgc atggatgtgt acacacccaa 780
gtcatcaaga caccatcaca cggatggcgc ctacttcggc actggtttcc ctcacatgct 840
cttcatgggtg catcccgagt accggcccaa gagacctgcc aaccagtttg tgcccaggct 900
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<210> 173

<211> 475

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(475)

<223> 3' terminal sequence. golgi apparatus
protein 1 (GLG1) gene.

<400> 173

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gggttttttt ctnaaaaaaa cctttgagtt gcaggtcagg tnagttgggt ctggaagtac 60
cggaagttct gttggnatga gagagacttg tctacaggca ggnaaacca agtttgccaa 120
acaaaggcag taaccccagc gaccagctgc tgctgctgca cggtaggag gaggaggaca 180
ccatggacac gagtggaggc tggatgggac aacgcagtg acatctgcta atg ctctaac 240
acgggggttg ngtcacttct gagaagagcg aggtnagtg ggatnctata caagagggt 300
ntacaaactg gggcactggg atagggtagt tcctttgggn gggtaagggt gggctctacc 360
ccgtccnttg agctctngtg tncactnccg ttgggggata cctcccaca cattcagggc 420
cantcaggna caattttacc aggtgntccc a ctgtttcac aggggggattt aagtt 475

```

<210> 174

<211> 483

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(483)

<223> 5' terminal sequence. golgi apparatus
protein 1 (GLG1) gene.

<400> 174

```

ggtcactctt tgccatgaagc tgagatatgc tgaccagcgc ctgtcttcag actgtgaaga 60
ccagatccga atcattatcc aggagtccgc cctggactac cgcctggatc ctcagctoca 120
gctgcactgc tcagacgaga tctccagtct atgtgctgaa gaagcagcag cccaagagca 180
gacaggtcag gtggaggagt gcc tcaaggc caacctgctc aagatcaaaa cagaattgtg 240
taaatnggaa gtgctaaaca tgctgaagga aagcaaagca gacatctttg ttgaccgggt 300
acttcatact tgcttgctgc ctgggacatt aaacaccact gcgcagcatt caccctgggc 360
cgcgggcggt caaattgttc ctgntttcat ggaaggcac tgggagggtt aaggcgggtt 420
gaggtttaca gcccgagttg caaaaaggcg cttcattgac ccggtttgag gtgttggtt 480
ttt 483

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<210> 175
<211> 3909
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3909)
<223> golgi apparatus protein 1 (GLG1) gene.

<400> 175
ggcacgaggc tcgccgcgga ctcaagatgg cggcgtgtgg acgtgtacgg aggatgttcc 60
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ccaggcgctc ccacagccag ggccagggtc cgggggcaa ctttgtgtcc ttcgtagggc 180
aggcgggagg cggcggcccg gcgggtcagc agctgcccc gctgcctcag tcatcgagc 240
ttcagcagca acagcagcag cagcaacagc aacagcagcc tcagccgccg cagccgcctt 300
tcccggcggg tgggcctccg cggcggggag gagcgggggc tgggtggggc tggaag ctgg 360
cggaggaaga gtcctgcagg gaggacgtga cccgcgtgtg ccctaagcac acctggagca 420
acaacctggc ggtgtctcag tgctgcagg atgtgagga gcctgaaaat gaaatttctt 480
cagactgcaa tcatttgttg tggaattata agctgaacct aactacagat cccaaatttg 540
aatctgtggc cagagagggt tgcaaatcta ctat aacaga gattaaagaa tgtgctgatg 600
aaccggttgg aaaagggttac atggtttcct gcttagtgga tcaccgaggc aacatcactg 660
agtatcagtg tcaccagtac attaccaaga tgacggccat catttttagt gattaccgtt 720
taatctgtgg ctctcatggat gactgcaaaa atgacatcaa cattctgaaa tgtggcagta 780
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gcctggtgaa agaagcagaa gaaagagaac ccaagattca agtttctgaa ctctgcaaga 900
aagccattct cgggttggtc gagctgtcat cggatgactt tcaacttagac cggcatttat 960
attttgcttg ccgagatgat cgggagcgtt tttgtgaaaa tacacaagct ggtg agggca 1020
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ctggtgcaga ttaccgcatt gatcgagctt tgaatgaagc ttgtgaatct gtaatccaga 1560
cagcctgcaa acatataaga tctggagacc caatgatctc gtcgtgcctg atggaacatt 1620
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gttccgctgt gcaatatggc aacgctcaga ttatcgaatg tctgaaagaa aacaagaagc 2580
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cagagctaga ctacaccctc atgagggtct gcaagcagat gataaagagg ttctgtccgg 2700

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aagcagattc taaaaccatg ttgcagtgt tgaagcaaaa taaa aacagt gaattgatgg 2760
atcccaaagt caaacagatg ataaccaagc gccagatcac ccagaacaca gattaccgct 2820
taaaccatcat gttaagaaaa gcctgtaaag ctgacattcc taaattctgt cacggatatcc 2880
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caaccctgtg ttagagcatt agcagatgtc cactgcgttg tcccatccag cctccactcg 3720
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tgcctttgtt tggcaaacct gggtttacct gcctgtagac aagtct ctct cataccaaca 3840
gaacttcggt tacttccaga accaactcac ctgacctgca actcaaaggc tttttaaga 3900
aaaccacca
3909

```

<210> 176

<211> 390

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(390)

<223> 5' terminal sequence. endothelin receptor
type b (EDNRB) gene.

<400> 176

```

gttaagatca aacctcaca agagaaatag aatgtttgaa aggctatccc aaaagacttt 60
tttgaatctg tcatcacat accctgtgaa gac aatacta tctacaattt ttccaggatt 120
attaaaatct tctcttttca ctatcgtagc ttaaactctg tttggttttg tcatctgtaa 180
atacttacct acatacactg catgtagatg attaaatgag ggcaggccct gtgctcatag 240
ctttacgatg gagagatgcc agtgacctca taataaagac tgtggaactg cctgggtgca 300
gtgtccacat gacaaagggg caggtaggca ccctctcttc acccatgctg tgggttaaat 360
gggtttctag gcatatgtat tatggctatt
390

```

<210> 177

<211> 4286

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4286)

<223> endothelin receptor type b (EDNRB) gene.

<400> 177

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 aggtaggcat ttgccccggt gggacgcctt gccagagcag tgtgtggcag gcccccggtg 120
 aggatcaaca cagtggctga ac actgggaa ggaactggta cttggagtct ggacatctga 180
 aacttggctc tgaactgcg cagcggccac cggacgcctt ctggagcagg tagcagcatg 240
 cagccgcctc caagtctgtg cggacgcgcc ctggttgccg tggttcttgc ctgoggccctg 300
 tcgcggtatc ggggagagga gagaggcttc ccgcctgaca gggccactcc gcttttgcaa 360
 accgcagaga taatgacgcc acccactaag accttatggc ccaagggttc caacgccagt 420
 ctggcgcggt cgttggcacc tgcgagggtg cctaaaggag acaggacggc aggatctccg 480
 ccacgcacca tctccctccc cccgtgccaa ggacccatcg agatcaagga gactttcaaa 540
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 cttctgagaa ttatctacaa gaacaagtgc atgcgaaacg gtcccaatat cttgatcgcc 660
 agcttggctc tgggagacct gctgcacatc gtcattgaca tccctatcaa tgtctacaag 720
 ctgctggcag aggactggcc atttggagct gagatgtgta agctggtgcc tttcatacag 780
 aaagcctccg tgggaatcac tgtgctgagt ctatgtgctc tgagtattga cagatatcga 840
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 attgttttga tttgggtggt ctctgtggtt ctggtgtccc ctgaagccat aggttttgat 960
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 gccaaaaccg tcttttgcct ggtccttgtc ttggccc tct gctggcttcc ccttcacctc 1260
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 gcaggtagca ccctctctca cccatgctgt ggttaaaatg gtttctagca tatgtataat 2700
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 gggttggagg aaacccatgg ggacagattc ccattcttag cctaacgttc gtcattgcct 3060
 cgtcacatca atgcaaaagg tccctgatttt gttccagcaa aacacagtgc aatgttctca 3120
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 atgtttctgt tcaatattga atgtgatggt acagtaaaacc aaaacccaac aatgtggcca 3300
 gaaagaaaga gcaataataa ttaattcaca caccatattg attctattta taaatcacc 3360
 acaaaactgt tctttaattt catcccaatc actttttcag aggcctgtta tcatagaagt 3420
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 tctgataacc ctttcttctt ccatgtcagt atcatgttct ctaattatct tgccaaattt 3600
 tgaaactaca caciaa aaagc atacttgcatt tattttataat aaaattgcatt tcagtggctt 3660

117/292

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tttaaaaaaa atgtttgatt caaaacttta acatactgat aagtaagaaa caattataat 3720
ttctttacat actcaaaacc aagatagaaa aagggtgctat cgttcaactt caaaacatgt 3780
ttcctagtat taaggacttt aatatagcaa cagacaaaaat tattgttaac atgg atgta 3840
cagctcaaaa gatttataaa agattttaac ctattttctc ccttattatc cactgctaata 3900
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tttattatgt aagcaaaacc aataaaaatt taagtttttt taacaactac cttatttttc 4140
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aaaatgccac atttctggtc tctggg 4286

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<210> 178

<211> 462

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(462)

<223> 3' terminal sequence. gran zyme b (granzyme
2, cytotoxic t-lymphocyte-associated serine
esterase 1) (GZMB) gene.

<400> 178

```

acancagaga tccatttatt acagtctctgc aaccccgact gccacccct tgggaattct 60
tgcctctgtc ccagagatgg tcaggcccag aggaagggtta gtctcatgcc tgctgttaga 120
ggcgnntcat tgttctcttt atccagggca ggaagtntga gaccttgatg tagactcctg 180
ggggtgtccc tttttgttt ccataggaga gaataccttg ggctangtcc ttacananga 240
ggggccccc ggagttcccc cttgaaaccg gtctgtgtct tctttggatc cccacacaa 300
atntcagtgg gctctgtctgt aattgcoatg ggaaggagac gggtcac ant gggcagttcc 360
ttctgcactn ttcaggaaca atttctgaa gtgtgggttg ctaaagtgtc cattgagaaa 420
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```

<210> 179

<211> 960

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(960)

<223> granzyme b (granzyme 2, cytotoxic
t-lymphocyte-associated serine esterase 1) (GZMB)
gene.

<400> 179

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agcagctcca accagggcag ccttcctgag aagatgcaac caatcctgct tctgtggcc 60
ttctcctctgc tgccagggc agatgcaggg gagatcatcg ggggacatga ggccaagccc 120
cactcccgcc cctacatggc ttatcttatg atctgggatc agaagtctct gaagaggtgc 180
ggtggttcc tgatacaaga cgacttcgtg ctgacagctg ctactgttg gggaagctcc 240
ataaatgtca cttgggggc ccacaatatc aaagaacagg agcc gaccca gcagtttatc 300
cctgtgaaaa gaccatccc ccatccagcc tataatccta agaacttctc caacgacatc 360

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118/292

atgctactgc agctggagag aaaggccaag cggaccagag ctgtgcagcc cctcaggcta 420
cctagcaaca aggcccaggt gaagccaggg cagacatgca gtgtggccgg ctgggggcag 480
acggccccc tgggaaaaca ct cacacaca ctacaagagg tgaagatgac agtgcaggaa 540
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ggggaccag agattaaaaa gacttccttt aagggggact ctggaggccc tcttgtgtgt 660
aacaaggtgg cccagggccat tgtctcctat ggacgaaaca atggcatgcc tccacgagcc 720
tgcaccaaag tctcaagctt tgtacactgg ataaagaaaa ccatgaaacg ctactaacta 780
caggaagcaa actaagcccc cgctgtaatg aaacaccttc tctggagcca agtccagatt 840
tacactggga gaggtgccag caactgaata aatacctctc ccagtgtaaa tctggagcca 900
agtccagatt tacactggga gaggtgccag caactgaata aa tacctctt agctgagtgg 960

<210> 180

<211> 471

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(471)

<223> 3' terminal sequence. fibroblast growth
factor receptor 1 (fms-related tyrosine kinase 2,
pfeiffer syndrome) (FGFR1) gene.

<400> 180

tnaagcagca gcaattttta ttgagggacc taaactgaaa ataggtttag aacataatTT 60
aaaaaataa aacagcaaaa gtagcaaaaa atatatgacc tttttaaaaa cattttcctt 120
ttttttcttt tttgttttta atatatagca actga tgcct cccagccacc agngcatct 180
taccgatgg gtaaatctct ggtaacgacc cttttaaaaa gacatgtaaa tatatactca 240
gntttataca ctttgtgttt tcttcatagc tatntacaga gccccagtt tgggctgggc 300
caggggcan caacactgcc cccaacctgg gccttcgcct caccatctc tgggtaccgg 360
gntttgggt caggcaaaagc aaactagtnt cgggtttatt angccactgg naccacctt 420
ttgggggcag aggtcacctt cattcgaggg cacgangcac tgacctcctt t 471

<210> 181

<211> 463

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(463)

<223> 5' terminal sequence. fibroblast growth
factor receptor 1 (fms-related tyrosine kinase 2,
pfeiffer syndrome) (FGFR1) gene.

<400> 181

gctttgtgc cagccacttc atccccctcc agatgttga ccaacacccc tccctgccac 60
caggactgcc tgannggagg agtgggagcc aatgaacagg catgcaagt agagcttct 120
gagctttctc ctgtcggttt ggtctgttt gccttcaccc ataagcccct cgactntgg 180
tggcaggtgc cttgtcctca gggctacagc agtagggagg tcagtgtctc gtgcctcgat 240
tgaagtgac ctctgcccc gataggtggg gccagtggct ttattaat tc cgatactagt 300
ttgctttgct gaccaaagtc ctgggtacca gaggatgggt aggcgaaggc aggttggggg 360
cagtgttgg gcccnggggc agcccaaaac tgggggcttc tgtatatagc tattgaagaa 420

aacacaaatg tattaatctg agtatatatt ttacatgtnt ttt

463

<210> 182

<211> 4066

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4066)

<223> fibroblast growth factor receptor 1

(fms-related tyrosine kinase 2, pfeiffer syndrome)

(FGFR1) gene.

<400> 182

cctcttgcgg ccacaggcgc ggcgtcctcg gcggcgggcg gcagctagcg ggagccggga 60
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cgcaggggcga tggagccggg ctgcaaggaa agtgaggcgc cgcgcgtcgc ttctggagga 360
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ccggggcacc agctccggtt ccattgttcc cgccgggct ggaggcgccg agcaccgagc 480
gccgcgggga gtcgagcgcc ggccgcggag ctcttgcgac ccgcgcagga ccggaacaga 540
gcccgggggc ggcgggcccg agccggggac gcgggcacac gccgcgtcgc acaagccacg 600
gcggactctc ccgaggcgga acctccacgc cgagcgaggg tcagtttgaa aag gaggatc 660
gagctcactg tggagtatcc atggagatgt ggagccttgt caccaacctc taactgcaga 720
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gtcatcgtgg agtatgcctc caagggaac ctgcgggagt acctgcaggc ccggaggccc 2460
ccagggctgg aatactgcta caacccagc cacaaccag aggagcagct ctccctcaag 2520

120/292

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gacctggtgt cctgcgccta ccaggtggcc cgaggcatgg agtatctggc ctccaagaag 2580
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catcgactac tataaaaaa caaccaacgg ccgactgcct gtgaagtgga tggcaccoga 2760
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tttttgctac ttttgctgtt ttattttttt aaattatgtt ctaaac 4066

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<210> 183

<211> 415

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(415)

<223> 5' terminal sequence. protein phosphatase 2
(formerly 2a), catalytic subunit, alpha isoform
(PPP2CA) gene.

<400> 183

```

cagttatata cctccatcac tagctggtga gctctagaca ccaacgtgag gccattggat 60
tgattaaatg tctcagaaat atcttgccca aagtgtaac cagctcctcg aggagatata 120
ccccaaccac caggtgcatc tggatctgac cacagcaagt cacacattgg accctcatgg 180
ggaacttctt gtaggcgata aagtgtctctg atatgatcca gtgtat ctat agatggcgag 240
agaccacatg gtagacagaa gatctgccc tccaccaagg cagtgaagg aagatagtca 300
aaaagatctg taaaatattt ccaaacattt ggcatttcca tattttctta aacattcatt 360
ctaggaaacc ttaacttgt gtgnatctgt cnggtcttct ggtttcctg gagga 415

```

<210> 184

<211> 2181

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

121/292

<220>

<221> misc_feature

<222> (1)..(2181)

<223> protein phosphatase 2 (formerly 2a),
catalytic subunit, alpha isoform (PPP2CA) gene.

<400> 184

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agagagccga gctctggagc ctcagcgagc ggaggaggag gcgcagggcc gacggccgag 60
tactgcggtg agagccagcg ggccagcgcc agcctcaaca gccgccagaa gtacacgagg 120
aaccggcgcc ggctgtgtcg ttaggcccgc tgtgcgggcg gcggcgcggg aggagcgcg 180
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tctgcgagaa ggctaaagaa atcctgacaa aagaatccaa cgtgcaagag gttcgatgtc 360
cagttactgt ctgtggagat gtgcatgggc aatttcatga tctcatggaa ctgtttagaa 420
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ccaatggcct caggttgggt tctagagctc accagctagt gatggaggga tataactggt 960
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aacttcagga tttatttgta tttcacatat tacaatttgt cacattgttg gtgtgcactt 2040
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agacttaatt gtaaaacat ataacttgag atttaagtct ttgggttggt ttttaataaa 2160
acagcatggt ttcaggtaga g                                     2181
```

<210> 185

<211> 375

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(375)

<223> 5' terminal sequence. homo sapiens, clone
image:4054156, mrna, partial cds (EST R55460)
gene.

122/292

<400> 185

cgaagaggat gaggaagagc tncgtgtgct gcancaagag ctccaggccg ggctgcgcac 60
caaggccctg attgtggatg agtcctgccg gcgtnacca tcttccaaca tagggatata 120
cctccctcct tcttataact gaagatcctg gagcccgaa gattcag ggc agacagaccc 180
tgataatgag cctggcaggg aagggaacc aacatcttgt aacttgcttt cccaccctg 240
tttctggggg cagagcaatt gcccaatttc taccctaate caaagtcctt ggggtgnggt 300
ggggttaaac gtgctggtgc atcctaggtc atccaagagt gaggcgcaa gtctctgagg 360
aagggggcac agaac 375

<210> 186

<211> 542

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(542)

<223> 3' terminal sequence. immunoglobulin kappa
constant (IGKC) gene.

<400> 186

gcaaagattc acaatattta ttnattctcc tccaacatta gcataattaa agccaaggag 60
gaggagggg gtgaggtgaa agatgagctg gaggaccgca ataggggtag gtcccctgtg 120
gaaaaagggt cagaggccaa aggatgggag ggggtcaggc tgganctgag gagcaggtgg 180
gggcacttct ccttctaaca ctctcccctg ttgaagctct ttgtgacggg cgagctcagg 240
ccctgatggg tgacttcgca ggcgtagact ttgtgtttct cgtagtctgc ttgtgctcagc 300
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ctgggggant taccnattt gggaggggcgt tatccacctt cactgtact ttggc ctctc 420
tggggataga agtttttca gcaggcacac aacagaggca nttocagatt tncaactgct 480
catcatgag cggggaagnt gaaggnacgt nggtgcagcc acattncctt tgatccncca 540
ct 542

<210> 187

<211> 296

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(296)

<223> 5' terminal sequence. melanocortin 1
receptor (alpha melanocyte stimulating hormone
receptor) (MCLR) gene.

<400> 187

atcacctgca gctccatgct gtccagcctc tgcttctggt gcgccatgc gtggaccgct 60
acatctccat cttctacgca ctgnctacca cagcatcgtg accctgccgc gggcggaag 120
nccgttgagg ccatctgggt ggccagtgtc gtcttcagca cgctcttcat cgcctactac 180
gaccacgtgg ccgtcctgct gtgcctcgtg gtctcttcc tggctatgct ggtgctcatg 240
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<210> 188

123/292

<211> 1270
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1270)
<223> melanocortin 1 receptor (alpha melanocyte
stimulating hormone receptor) (MCLR) gene.

<400> 188
ggagaggggtg tgagggcaga tctgggggtg cccagatgga aggaggcagg catggggggac 60
accaagggcc ccctggcagc accatgaact aagcaggaca cctggagggg aagaactgtg 120
gggacctgga ggcctccaac gactccttcc tgcttcctgg acaggactat ggctgtgcag 180
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gggctggctg ccaaccagac aggagcccg ggcctggagg tgtccatctc tgacgggctc 300
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ctgctggtga gcgaggagaa cgtgctggag acggccgtca tctcctgct ggaggccggt 480
gcactggtgg cccgggctgc ggtgctgcag cagctggaca atgtcattga cgtgatcacc 540
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aagtgtgctg ggcagagggg ggtggtgata ttgtgtggtc tggttcctgt gtgaccctgg 1200
gcagttcctt acctccctgg tccccgtttg tcaaagagga tggactaaat gatctctgaa 1260
agtgttgaag 1270

<210> 189
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(336)
<223> 3' terminal sequence. neuregulin 1 (NRG1)
gene.

<400> 189
ccaanaccaa atccgagccc ttggacaaa ctgcctgcg ccgagagccg tccgcgtaga 60
gcctccgtct ccggcgagat gtccgagcgc aaagaaggca gaggcaaagg gaagggcaag 120
aagaaggagc gaggtctcnc aagaagccgg ntccgggggc ggngcagcag gagcccagcc 180
ttgcctcccc aattnaaaga gatgaaaagc caggaatcgg ctgcaggttc caaactagtc 240
cttcggtgtg aaaccagttc tgaatactcc tctctcagat tcaagtgggt caagaatggg 300
gaatgaattg aatcgaaaaa nncannccac aaaatt 336

124/292

<210> 190
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(366)
<223> 5' terminal sequence. neuregulin 1 (NRG1)
gene.

<400> 190
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cattctcggg gggtnngtta g gatggtgag gccattggc aatgttcac atattgtttc 120
gttcagaccg aagctctgcc agagacggtc atgcagcttt ttccgctgtt tcttggtttt 180
gcagtaggcc accacacaca tgatgccgac cacaaggagg gcgatgcaga tgccggttat 240
ggtcagcaact ctcttctggt acagctcctn cgcctncata aattcaatnc caagatgctt 300
gtagaagctg gccattnacg tagttttttg gcagcgattc accagtaaaa cttcatttng 360
gggcac 366

<210> 191
<211> 2490
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2490)
<223> neuregulin 1 (NRG1) gene.

<400> 191
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cgggctcggc cggaggccag gagctgag cg gcggcggctg ccggacgatg ggagcgtgag 120
caggacggtg ataacctctc cccgatcggg ttgcgagggc gcggggcaga ggccaggacg 180
cgagcccgcca gcggcgggac ccacgcagca ctcccgggg cgacaggagc agccccgaga 240
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cagaggcaaa ggaaggggca agaagaagga gcgaggctcc ggcaagaa gc cggagtccgc 540
ggcgggcagc cagagcccag ccttgcctcc ccaattgaaa gagatgaaa gccaggaaac 600
ggctgcagggt tccaaactag tccttcgggt tgaaaccagt tctgaatact cctctctcag 660
attcaagtgg ttcaagaatg ggaatgaatt gaatcgaaaa aacaaaccac aaaatatcaa 720
gatacaaaaa aagccaggga agtcag aact tcgcattaac aaagcatcac ttgctgattc 780
tgagagatg atgtgcaaag tgatcagcaa attaggaaat gacagtgcct ctgccaatat 840
caccatcgtg gaatcaaacg agatcatcac tggatgcca gcctcaactg aaggagcata 900
tgtgtcttca gactctccca ttagaatatc agtatccaca gaaggagcaa atactcttc 960
atctacatct acatccacca ctgggacaag catcttgtta aaatgtgcgg agaaggagaa 1020
aactttctgt gtgaatggag gggagtgtt catggtgaaa gacctttcaa accctcagag 1080
atacttgtgc aagtgcctaa atgagtttac tgggtgatgc tgccaaaact acgtaatggc 1140
cagcttctac aaggcggagg agctgtacca gaagagagt ctg accataa ccggcatctg 1200
catcgccctc cttgtgggtc gcacatgtg tgtgggtggc tactgcaaaa ccaagaaaca 1260
gcggaaaaag ctgcatgacc gtcttcggca gagccttcgg tctgaacgaa acaatatgat 1320
gaacattgcc aatgggcctc accatcctaa cccaccccc gagaatgtcc agctggtgaa 1380

125/292

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tcaatacgtat tctaaaaa cg tcattctccag tgagcatatt gttgagagag aagcagagac 1440
atcctttttcc accagtcaact atactttccac agcccatcac tccactactg tcaccagagac 1500
tcctagccac agctggagca acggacacac tgaaagcatc ctttcgaaa gccactctgt 1560
aatcgtgatg tcatccgtag aaaacagtag gcacagcagc ccaactgggg gcccaag agg 1620
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ggaaatgtct ccaccgtgt ccagcatgac g gtgtccaag ccttccatgg cggtcagccc 1860
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cagcctccct gctagcccct tgaggatagt ggaggatgag gagtatgaaa cgaccaaga 2040
gtacgagcca gcccaagagc ctgttaagaa actcgccaat agccggcggg ccaaaagaac 2100
caagcccaat ggccacattg ctaacagatt ggaagtggac agcaacacaa gctcccagag 2160
cagtaactca gagagtgaaa cagaagatga aagagtaggt gaagatacgc ctttcctggg 2220
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caggactaac ccagcaggcc gcttctcgac acaggaagaa atccaggcca ggctgtctag 2340
tgtaattgct aaccaagacc ctattgctgt ataaaaccta aataaacaca tagattcacc 2400
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ttagcagttc tgcaataaaa aaaaaaaaaa 2490

```

<210> 192
 <211> 453
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(453)
 <223> 5' terminal sequence. ciliary neurotrophic
 factor receptor (CNTFR) gene.

```

<400> 192
cagatgctac gccgggaagg agtacattat ccagggtggca gccaaaggaca atnagattgg 60
gacatggagt gactggagcg taccgcccac gctacgccct ggactgagga accgcgacac 120
ctcaccacgg aggccaggc tgcgagagacc acgaccagca ccaccagctc cctggcacc 180
ccacctacca cgaagatctg tgaccctggg gagctgggca gcggcgggg accctcggca 240
cccttcttgg tcagcgctcc catcactctg gccctggctg ncgctgcgc cactgccagc 300
agtccttga tctgagccc gcacccatg aggcacatga gagcacctgc agaggancag 360
gaggccggag cttgagcctt gtgaccccg gtttctattt tncacacggg caggaggant 420
ttttgcattn tttttnagac acaatttttt gga 453

```

<210> 193
 <211> 1566
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(1566)
 <223> ciliary neurotrophic factor receptor (CNTFR)
 gene.

<400> 193

126/292

```

gcggcgccag cggaggcgcc ggctccagcc ggcgcgccgc gaggctcggc ggtgggatcc 60
ggcggggcgg gctagctccg cgtccctgc ctgctcgtct gccggggcg gtcggaagcc 120
gcggcgcgaa gcccggttg cccgaggcg cgactct agc cttgtcacct catcttgccc 180
ccttggtttt ggaagtccctg aagagttggt ctggaggagg aggaggacat tgatgtgctt 240
ggtgtgtggc cagtgttgaa gagatggctg ctctgtccc gtgggcctgc tgtgtgtgc 300
ttgcgcgcgc cgcgcagtt gtctacgcc agagacacag tccacaggag gcaccccatg 360
tgcagtaaga gcgcc tgggc tctgacgtga cactgccatg tgggacagca aactgggatg 420
ctgcggtgac gtggcggtta aatgggacag acctggcccc tgacctgctc aacggtcttc 480
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tgctcagctg ccgctccaac acttacccca agggcttcta ctgcagctgg catctgcca 660
ccccaccta cattccaac accttcaatg tgactgtgct gcatggctcc aaaattatgg 720
tctgtgagaa ggacccagcc ctcaagaacc gctgccacat tgcctacatg cactgttct 780
ccaccatcaa gtacaaggtc tccataagtg tcagc aatgc cctggggccac aatgccacag 840
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ggctcagccc cagcaacctg cgccggttg aggtgacgtg gcagacccc tcgacctggc 960
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agcctgcaga ccccggtttc tatttt gcac acgggcagga ggacctttg cattctcttc 1500
agacacaatt tgtggagacc ccggcgggcc cgggcctgcc gccccccagc cctgccgcac 1560
caagct 1566

```

<210> 194

<211> 349

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(349)

<223> 5' terminal sequence. angiogenin,
ribonuclease, rnase a family, 5 (ANG) gene.

<400> 194

```

ccgtgtacac aactcacac aaggacgcca accccaccta gatgcaaaga ggattcaaaa 60
gaacatcttt cgtttttcta ccggtccccc atcatcgtac tagggaggaa gaagcgggtg 120
agaaacaaaa cttttttcca ttgtcctgcc cgtttctgcg gacttgttct gaggccgagg 180
agcctgtggt ggaagagatg gtgatgggcc tgggcgtttt gttgttggtc ttcgtgctgg 240
gtctgggtct gacccaccg acctggctc aggataactn c aggtacaca cacttctga 300
cccagcacta tgatgcaaaa ccacagggcc ngggatgaca gatactgtg 349

```

<210> 195

<211> 729

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature
<222> (1)..(729)
<223> angiogenin, ribonuclease, rnase a family, 5
(ANG) gene.

<400> 195
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ttgggtctac cacacctcct ttgcccctcc gcaggagcct gtgttggaag agatgggtgat 120
gggcctgggc gttttgttgt tggctctcgt gctg ggtctg ggtctgacct caccgaccct 180
ggctcaggat aactccaggt acacacactt cctgacctag cactatgatg ccaaaccaca 240
gggcccggat gacagatact gtgaaagcat catgaggaga cggggcctga cctcaccctg 300
caaagacatc aacacattta ttcattggca caagcgcagc atcaaggcca tctgtgaaaa 360
caagaatgga aaccctcaca gagaaaacct aagaataagc aagtcttctt tccagggtcac 420
cacttgcaag ctacatggag gttcccctcg gcctccatgc cagtaccgag ccacagcggg 480
gttcagaaac gttgttggtt cttgtgaaaa tggcttacct gtccacttgg atcagtcaat 540
tttccgtcgt ccgtaaccag cgggcccctg gtcaagtgtt ggctctgctg tcct tgcctt 600
ccatttcccc tctgcaccca gaacagtgtt ggcaacattc attgccaagg gcccaaagaa 660
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gatatcagt 729

<210> 196
<211> 452
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(452)
<223> 3' terminal sequence. endoglin
(osler-rendu-weber syndrome 1) (ENG) gene.

<400> 196
ngttactcca gccttgagacc ggggctgcca ctt ggagagn cgtggcgacc acaaggaggc 60
gcacatcctg agggctcctgc cgggccactc ggcgggcccc ggacgggtga cgggtgaagg 120
ggaactgagc tgccgacccg gggatctcga tgcgctcctc atcctgcagg gtccccctta 180
cgtgtcctgg ctcatcgacg ccaaccacaa catgcagatc tggaccactg gagaatactc 240
cttcaagatc tttccagaga aaaacattcg tggcttcaag ctcccagaca cacctcaagg 300
cctcctgggg ggacgcgngn atgcttcaat gccagcattg tggcatcctt cgtgggagct 360
taccgctggg ccagcattgt cttnatattca ttgccttcca gcttgcggtt gttagggttg 420
cagaccttaa ccgnaccgt ttccagacca tt 452

<210> 197
<211> 379
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(379)
<223> 5' terminal sequence. endoglin
(osler-rendu-weber syndrome 1) (ENG) gene.

<400> 197

128/292

```

aggacgagc ctttgcttgt gcaaccagac aggtcagggc tgatgatgtt caagcgcattg 60
aagacagtcc tatggcttcc tggcttgag acccggtctt gggacgcagg gctaccgtgc 120
agctgagggg gccggttttg ggtatgggta ctgtgtagaa gtggaggagg aagctgaagc 180
gcgggtcacc ctcggggctt ggggacagca ggct cacaca gttgcccttg gccgcccggc 240
cctgggatga gttccacggt gcctccctca ggcccaagt ccagggtggc agctgtctaa 300
ctggagcagg aactcggaga cggatgggga cantctgacc tgcacaaagc tttntttgcc 360
ccggcttcga tgggtgtttt                                     379

```

<210> 198

<211> 3142

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3142)

<223> endoglin (osler-rendu-weber syndrome 1)
(ENG) gene.

<400> 198

```

cctgggcccgg ccgggctgga tgagccgg ga gctccctgct gccggtcata ccacagcctt 60
catctgcgcc ctggggccag gactgtgtgt gtcactgcca tccattggag ccagcacc 120
cctcccggcc catccttcgg acagcaactc cagcccagcc ccgcgtccct gtgtccactt 180
ctcctgaccc ctcgggccgg accccagaag gctggagcag ggacgccgtc gctccggccg 240
cctgctcccc tcgggtccccc gtgcgagccc acgcccggccc cggtgcccgc ccgcagccct 300
gccactggac acaggataag gccagcgca caggccccc cgtggacagc atggaccgcg 360
gcacgctccc tctggctgtt gccctgtgc tggccagctg cagcctcagc cccacaagtc 420
ttgcagaaac agtccattgt gaccttcagc ctgtggggcc cgagagggg c gaggtgacat 480
ataccactag ccagggtctcg aagggtgtcg tggctcaggc ccccaatgcc atccttgaag 540
tccatgtcct ctccctggag ttcccaacgg gcccgtcaca gctggagctg actctccagg 600
catccaagca aaatggcacc tggcccggag aggtgcttct ggtcctcagt gtaaacagca 660
gtgtcttctc gcatctccag gccctgg gaa tcccactgca cttggcctac aattccagcc 720
tggtcacctt ccaagagccc ccgggggtca acaccacaga gctgccatcc ttcccaaga 780
cccagatcct tgagtgggca gctgagaggg gcccacacac ctctgtgtgt gagctgaatg 840
accccagag catcctctc cgactgggcc aagcccaggg gtcactgtcc ttctgcatgc 900
tggaagccag ccaggacatg ggccgcacgc tgcagtggcg gccgcgtact ccagccttgg 960
tccggggctg ccacttgaa ggcgtggccg gccacaagga ggccacatc ctgaggggtcc 1020
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gcaaaggcct cgtcctgccc gccgtgctgg gcatcacctt tgggtgccttc ctcatcgggg 2160
ccctgctcac tgctgcactc tggtagatct actgcacac gcgtgag tac ccaggcccc 2220

```

129/292

```
cacagtgagc atgccggggc cctccatcca cccgggggag cccagtgaag cctctgagg 2280
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tggtaccagc actggtgaac tgagctggg aggaaggag aacttgaac agattcaggc 2820
cagcccagcc aggccaacag cacctcccc ctggg aagag aagagggcc agccagagc 2880
cacctggatc tatcctgcg gctccacac ctgaacttg ctaactaact ggcaggggag 2940
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ggagcctagc tctgccaca tggagcccc tctgccggtc gggcagccag cagaggggga 3060
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tgaaacctga aaaaaaaaaa aa 3142
```

<210> 199
<211> 402
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(402)
<223> 3' terminal sequence. epidermal growth
factor (beta-urogastrone) (EGF) gene.

```
<400> 199
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acaaatcagg caatttactt acaatcttgt aactgaaat acatacaaa t tctgtgcaat 120
cacaccaaga gggaaaattc tgtaggggaa agggacagta atgactaaga aactccgaag 180
cctcctgtgt aatattttta aaataaaatg ttttcattca aatattttta aaaataagcc 240
atctaattct gaagaaatca gtttctaaat tacatttttc attgattcat cacaactcat 300
tttgcaaat catcagcatg gaccacg cca atgaggagtt aaatgcctac actgtatott 360
aacggtattg taatattcca atcatttcac gaaactgata ta 402
```

<210> 200
<211> 4877
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(4877)
<223> epidermal growth factor (beta-urogastrone)
(EGF) gene.

```
<400> 200
actgttggga gaggaatcgt atctccatat ttcttctttc agccccaatc caagggttgt 60
agctggaact ttccatcagt tcttcctttc ttttctctct ctaagccttt gccttgcct 120
gtcacagtga agtcagcca g agcagggtg taaactctg tgaaatttgt cataagggtg 180
tcaggtattt cttactggct tccaaagaaa catagataaa gaaatctttc ctgtggcttc 240
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ccttggcagg ctgcattcag aaggtctctc agttgaagaa agagcttggg ggacaacagc 300
 acaacaggag agtaaaagat gcccagggc tgaggcctcc gctcaggcag ccgcatctgg 360
 ggtcaatcat actcaccttg cccgggccat gctccagcaa aatcaagctg ttttcttttg 420
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 cgcaggaaat gggaattcta ctgtgtggg tctgcacc c tcttaattt tctcccatgg 600
 aaatagtatc tttagattg acacagaagg aaccaattat gagcaattgg tgggtgatgc 660
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 ggcccactac tacaggactc agaagctgct atcgaaaaac ccaaagaatc cttatgagga 3660
 gtcgagcaga gatgtgagga gtcgcaggcc tgcgtgacact gaggatggga tgtcctcttg 3720
 ccctcaacct tggtttgttg ttataaaaga acaccaagac ctcaagaatg ggggtcaacc 3780
 agtggctggg gaggatggc aggcagcaga tgggtcaatg caaccaactt catggaggga 3840
 ggagccccag ttatgtggaa tgggcacaga gcaaggctgc tggattccag tatccagtga 3900

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```

taagggtcc tgtccccagg taatggagcg aagctttcat atgccctcct atgggacaca 3960
gacccttgaa gggggtgtcg agaagcccca ttctctccta tcagctaacc cattatggca 4020
acaaagggcc ctggaccac cacac caaat ggagctgact cagtgaaaac tggaattaaa 4080
aggaaagtca agaagaatga actatgtcga tgcacagtat cttttctttc aaaagtagag 4140
caaaactata ggtttttggt ccacaatctc tacgactaat cacctactca atgcctggag 4200
acagatacgt agttgtgctt ttgtttgctc ttttaagcag tctcactgca gtcttatttc 4260
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gtaaattgcc tgatttgttt tcattataga caacgatgaa tttcttctaa ttatttaaat 4860
aaaatcacca aaaacat
4877

```

<210> 201

<211> 153

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(153)

<223> 3' terminal sequence. hmt1 (hnrnp
methyltransferase, s. cerevisiae) -like 1 (HRMT1L1)
gene.

<400> 201

```

attagacctc acattaggga aaacatcaaa atgantcacg cagaccctt gagatcctga 60
ggttggccca gccgagcccg tgctcagaag cccccagct cgggccccca gctgcccgca 120
cgccccccct caccagcagg caggtcccca tcc
153

```

<210> 202

<211> 472

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(472)

<223> 5' terminal sequence. hmt1 (hnrnp
methyltransferase, s. cerevisiae) -like 1 (HRMT1L1)
gene.

<400> 202

```

agtgaatcgc agggagaaga gcctgctgag tncagtgagg cgggtctcct gcaggaggga 60
gtacagccag aggagtttgt ggccatcgcg gactacgctg ccaccgatga gaccagctc 120
agttttttga gaggagaaaa aattcttatc ctgagacaaa cactgcaga ttggtggtgg 180
ggtgagcgtg cgggctgctg tgggtacatt c cggcaaacc atgtggggaa gcacgtggat 240
gagtacgacc ccgaggacac gtggcaggat gaagagtact tcggcagcta tggaactctg 300

```

132/292

aaactccact tgggagatgt tggcagacca gccacgaaca actaaatacc acagtgttca 360
ttcctgnacg gaattaaaga atccctgnac ggnttaaagt tcttcnngg acgtggggct 420
gtggggattt gggatccntc agtctcttnt tgttgacat tttgcgtggc nt 472

<210> 203

<211> 2093

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2093)

<223> hmt1 (hmrnp methyltransferase, s.
cerevisiae)-like 1 (HRMT1L1) gene.

<400> 203

cactgcgctt gcgcgggttg agggcggttg ctacgtctcc tggaaaggac cgtccacccc 60
tccgcgcttg cgggtgtggac gcggaactca gcggagaaac gcgattgaga aatggaaaag 120
aaaatgaaat aaatcagcag ttatgaggca gagcctaaga gaactatggc aa catcaggt 180
gactgtccca gaagtgaatc gcaggagaa gagcctgctg agtgcagtga ggcgggtctc 240
ctgcaggagg gagtacagcc agaggagttt gtggccatcg cggactacgc tgccaccgat 300
gagaccagc tcagtttttt gagaggagaa aaaattctta tcctgagaca aaccactgca 360
gattgtgtgt ggggtgagcg tgcgggctgc tgtgggtaca ttccggcaaa ccatgtgggg 420
aagcacgttg atgagtacga ccccgaggac acgtggcagg atgaagagta cttcggcagc 480
tatggaactc tgaactcca cttggagatg ttggcagacc agccacgaac aactaaatac 540
cacagtgtca tctgcagaa taaagaatcc ctgacggata aagtcaccc tggacgtggg 600
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aggacgcacg catatcagcc cgtgtaccct gtgacagtga ctgtccccc ctcctgtgtt 1860
agtgtgccc ttactgccgt cgtcatcca ctggtgtggg acgtaggatt gcaca gggct 1920
gtgccagtgg cgtgtaggga aactgccct ggctcagcgt gcgagctaag gtggcgatgt 1980
atgcgatggg actctgcatg ggatagtaca gttgtgtaga cgtcttccaa ataaattatg 2040
tgttggtgcc atcgacatg ctcaataaat attttaaat agtgaaaaaa aaa 2093

<210> 204

<211> 431

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(431)

<223> 3' terminal sequence. ets variant gene 4
(ela enhancer-binding protein, elaf) (ETV4) gene.

<400> 204

```
tgggggcctt tatta aggtc tggcagatgt ggtggaggtg gaagtacaaa ccaggcctg 60
ggcctaggaa agggcagaag aaaggcaaag ggtcccttgg agcaggaacc catccctctc 120
tgcttatacc cagcaccct catccaggt tcctttcttc aacctccgcc tgcctctggg 180
aacacagagc accaagaact gacaaaccgg gaccctccag gggccacagc gtgggggc ag 240
agtccagggg ttctgtctcc ccgcagtggg gagatctngg ggagctcagg tgaacctcct 300
cancctcctg ccagtatgaa gttggggaag cgccttttct tgtccccag aacagaacaa 360
actcttggtc tctgtgggtt ngggggaaaa ggtttngggg ggtttgact taggggagaa 420
gttnagcttg a                                     431
```

<210> 205

<211> 435

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(435)

<223> 5' terminal sequence. ets variant gene 4
(ela enhancer-binding protein, elaf) (ETV4) gene.

<400> 205

```
gtccccctgcc cctgcccttg gacagtcgcc cctacagncc tttccccggg cagagaacgg 60
aatttctctga gatcctcttg cacctcccag cccaccctg gccatgggta cctcggggaa 120
catagctccg tcttcagca gccctggga catttgccac tccttcacat ctcaggagg 180
gggcccggaa cccctcccag gcccctacc aacaccagct gtcggagccc tgcccacct 240
atccccagca gagctttaag caagaatacc atgatccct gtatggaaca gggnggggcc 300
agccaggccg tgggaaccag ggtgggggt tcaatggggg cacagggtac ccaggggggn 360
gggggggttg ttgattcaaa acagggaaca gacgggattt tt ggnttaag gatttnaggt 420
tntttaancg gggtg                                     435
```

<210> 206

<211> 447

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(447)

<223> 5' terminal sequence. annexin a11 (ANXA11)
gene.

<400> 206

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```

agacccagct cctctttgac atttatgaga taaaggaagc catcaagggg gttggcactg 60
atgaagcctg cctgattgag atcctcgctt cccgcagcaa tgagcacatc cgagaattaa 120
acagagccta caaagcagaa ttcaaaaaga ccctggaaga ggcca ttcga agcgacacat 180
cagggcactt ccagcggtc ctcactcttc tctctcagg aaaccgtgat gaaagcacia 240
acgtggacat gtcactcgcc cagagagatg cccagggagc tgtatgcggn ccggggagaa 300
ccgcctgggg aacagacgag tccaagtttc aattgcggtt tctgtggctt cccgggagcc 360
gggcncacc tgggtaggca gtt tttcaat gagttaccag agaatgnaca gggcncggac 420
attntagaa gagcatctgc cgggaga 447

```

<210> 207

<211> 1958

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1958)

<223> annexin all (ANXA11) gene.

<400> 207

```

gctgctgcgc ccgcggtccc ccagtgcctc gagtgcctcg cgggccccgc gagcgggagt 60
gggacccagc cctaggcaga acccaggcgc cgcgccccgg acgccccgag agagagccac 120
tcccgccac gtccatttc gccctcgcg tccggagtcc ccgtggc cag atctaaccat 180
gagctaccct ggctatcccc cgcctccagg tggtaccaca ccagctgcac caggtggtgg 240
tccctgggga ggtgctgcct accctctccc gccagcatg ccccccacg ggctggataa 300
cgtggccacc tatgcggggc agttcaacca ggactatctc tcgggaatgg cggccaacat 360
gtctgggaca tttggaggag ccaac atgcc caacctgtac cctggggccc ctggggctgg 420
ctaccacca gtgccccctg gcggctttgg gcagcccccc tctgccagc agcctgttcc 480
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gccataccca ggggccccctg tgccgggcca gcccatgcca cccccggac agcagcccc 600
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cgtgtgccc ccaaccagct ttggaagccg aggcaccatc actgatgctc ccggctttga 780
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gtaccacgac atctcgggag atacttcagg ggattaccgg aagattctgc tgaagatctg 1680
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tcacctctct agagcttagg cctgtcttcc accctcctg acccgatatg tgtgccacag 1860
gacctggctc ggtctagaac tctctcagga tgccttttct accccatccc tcacagctc 1920
ttgctgctaa aatagatggt tcatttttct gaaaaaaa 1958

```

<210> 208

<211> 433

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(433)

<223> 5' terminal sequence. platelet-derived
growth factor receptor, beta polypeptide (PDGFRB)
gene.

<400> 208

```
gccagatgaa gcaaggccat ataccctaaa cttccatcct gggggtcagc tnggctcctg 60
ggagattcca gatcacacat cacactctgg ggactcagga accatgcccc ttccccaggc 120
ccccagcaag tctcaagaac acagctgcac aggccttgac ttagagtnac agccggtntc 180
ctggnaaagcc cccagcagct gccccaggga catgggaaga ccacgggacc tctttcacta 240
cccacgatga cctccggggg tctctggggg caaaaggagc aaagagggca aatgagatca 300
cctnctgcag cccaccactt ccagcacctg tgccgaggtt ttic gticga agacagaatt 360
ggacagttga ggacagttat tgtctttntt taaaagnaca aggaagggtt cagnttgggt 420
taccaccaag gag                                     433
```

<210> 209

<211> 5570

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5570)

<223> platelet-derived growth factor receptor,
beta polypeptide (PDGFRB) gene.

<400> 209

```
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agaccaggg cggccctctt ggcggtctg ctccctccga aggatgcttg gggagtgagg 120
cgaagctggg cgctcctctc ccctacagca gcccccttec tccatccctc tgttctcctg 180
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acaatgactc ccgtggactg gagaccgatg agcggaaacg gctctacatc tttgtgccag 720
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```


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 cttgacttag agtgacagcc ggtgtcctgg aaagccccaa gcagctgccc cagggacatg 4920
 ggaagaccac gggacctctt tcaactacca cgatgacctc cgggggtatc ctgggcaaaa 4980

137/292

```
gggacaaaga gggcaaatga gatcacctcc tgcagcccac cactccagca cctgtgccga 5040
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cttcagatgg taccccaaga aggatgtgag aggtggccgc ttggagtttg cccctcacc 5160
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gttggtccaa ggaggagag tgggttctca atacggtacc aaagatataa tcacctagg 5460
ttacaaatat ttttaggact cactttaact cacatttata ca gcagaaat gctattttgt 5520
atgctgttaa gtttttctat ctgtgtactt ttttttaagg gaaagatttt 5570
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<210> 210

<211> 406

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(406)

<223> 5' terminal sequence. williams-beuren
syndrome chromosome region 14 (WBSR14) gene.

<400> 210

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gaccggcgta tcacacacat ctccgcgga aggaagcggc gcttcaacat caagctgggg 60
tttgacaccc ttcattgggt cgtgagcaca ctgagtgccc agccagcct caaggtgagc 120
aaagctacca cgctgcagaa gacagctgag tacatcctta tgctacagca ggagcgtgcg 180
ggcttgacag aggaggccca gcagctgcgg gtagtgagatt gaggagctca atgccgccat 240
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accagatgcg agacatgttt gatggactac gtccgaacct gtacgctgca caa ctgggaa 360
gttctggggg ntttcagcat cctnattccg gcctctgttt tgagtc 406
```

<210> 211

<211> 3293

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3293)

<223> williams-beuren syndrome chromosome region
14 (WBSR14) gene.

<400> 211

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ccccgcgtg cgcggagcag ggaccaggcg gttgcggcgg cgacagccat ggccggcgcg 60
ctggcaggtc tggccgcggg cttgcaggtc ccgcgggtcg cgccagccc agactcggac 120
tcggacacag actcggagga cccgagctc cggcgagc g cgggcggctt gctccgctcg 180
caggtcatcc acagcgggtca cttcatggtg tcgtcgccgc acagcgactc gctgccccgg 240
cggcgcgacc aggaggggtc cgtggggccc tccgacttcg ggccgcgcag tatcgacccc 300
aactcacac gcctcttcga gtgcttgagc ctggcctaca gtggcaagct ggtgtctccc 360
aagtgaaga atttcaa agg cctcaagctg ctctgcagag acaagatccg cctgaacaac 420
gccatctgga gggcctggtg tatccagtat gtgaagcggg ggaagagccc cgtgtgtggc 480
ttcgtgaccc ccctgcaggg gcctgaggct gatgcgcacc ggaagccgga ggccgtggtc 540
ctggagggga actactggaa gcggcgcatc gaggtggtga tgcgggaata ccacaagtg g 600
```

138/292

```

cgcatctact acaagaagcg gctccgtaag cccagcaggg aagatgacct cctggccct 660
aagcaggcgg aaggcagggtg gccgccgcgg gagcaatggt gcaaacagct cttctccagt 720
gtgggtccccg tgctgtctggg ggacccagag gagagcggg gtgggcggca gctcctggac 780
ctcaattgct ttttgtccga catctcagac actctct tca ccatgactca gtccggccct 840
tcgcccctgc agctgccgccc tgaggatgcc tacgtcggca atgctgacat gatccagccg 900
gacctgagcg cactgcagcc aagcctggat gacttcatgg acatctcaga tttctttacc 960
aactccccgc tcccacagcc gcccatgcct tcaaacttcc cagagcccc cagcttcage 1020
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ttccctggg agaggccagg agggcctgat cccaggagac accagggcca gagtgaccac 3180
agcagggcag gcacatgtg tgtgtgtgtg tgtggatgtg tgtgtgtgg ttttgtaaag 3240
aattcttgac caataaaagc aaaaactgtc tgctgggtta aaaaaaaaaaaa 3293

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<210> 212

<211> 207

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(207)

<223> 5' terminal sequence. cd74 antigen

(invariant polypeptide of major histocompatibility
complex, class ii antigen-associated) (CD74) gene.

139/292

<400> 212

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cctttggcct tggcttttct agtcctatct acctgtcagg ctgagccatc tctcttccc t 60
ttccccagtc atcactcccc aaggaagagc caatgttttc caccataat cttttctgcc 120
gaccctagtc tccctctgct cagccaagct tggtatcagc ttccagggcc atngttcaca 180
ttagaataaa aggtagtaat taganaa 207
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<210> 213

<211> 1304

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1304)

<223> cd74 antigen (invariant polypeptide of major histocompatibility complex, class ii antigen-associated) (CD74) gene.

<400> 213

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ttcccagatg cacaggagga gaagcaggag ctgtcgggaa gatcagaagc cagtcattga 60
tgaccagcgc gaccttatct ccaacaatga gcaactgccc atgctgggccc ggccgacctgg 120
ggccccggag agcaagtga gccgcggagc cctgtacaca ggcttttcca tcttggtgac 180
tctgtctctc gctggccagg ccaccaccgc ct acttctctg taccagcagc agggccgggt 240
ggacaaactg acagtcaact ccagaaacct gcagctggag aacctgcgca tgaagcttcc 300
caagcctccc aagcctgtga gcaagatgag catggccacc ccgctgctga tgcaggcgct 360
gcccatggga gccctgcccc agggggcccat gcagaatgcc accaagtatg gcaacatgac 420
agaggaccat gtgatgcacc tgctccagaa tgctgacccc ctgaaggtgt acccgccact 480
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gaaggtcttt gagagctgga tgcaccattg gctcctgttt gaaatgagca ggcaactcctt 600
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tgggctgggt gtgaccaagc aggatctggg ccagtcgcc atgtgagagc agcagaggcg 720
gtcttcaaca tctgcccagc ccacacagc tacagctttc ttgctccctt cagccccag 780
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tcaccttgtt acaagacaaa ccaagtcgga acagcagata acaatgcagc aaggccctgc 900
tgcccaatct ccatctgtca acaggggctg gaggtcacc gaagtggcca aaagctagac 960
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ggaccataa tctttctgct cgaccctag ttccctctgc tcagccaagc ttgttatcag 1260
ctttcagggc catggttcac attagaataa aaggtagtaa ttag 1304
```

<210> 214

<211> 355

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(355)

<223> 5' terminal sequence. annexin a7 (ANXA7) gene.

<400> 214
aggaaactatc cgaccagctg ccaacttcga tgctataaga gatgcagaaa ttcttcgtaa 60
ggcaatgaag ggttttgagg caagatgagca ggcaattgtg gatgtngttg ccaaccgttt 120
ccaatgatca gaggcaaaaa attaaagcag catttaagac ctccataggg aaggatttaa 180
tcaaagatct caaatcagag ttaagtingaa atatggaaga actgatcctn ggccctcttc 240
atgcctccta cgtattacga tgcctngagc tttacggaaa gcaatncagg gancaggtac 300
tcaggancgt tgtattttgat ttnggatttt ngtgacang atcanattca ggtaa 355

<210> 215
<211> 2176
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2176)
<223> annexin a7 (ANXA7) gene.

<400> 215
gaaccgcgtc tcccgaaga tggagccggg ttgggctgtg acgctgctgc tggggtcaga 60
atgtcatacc caggctatcc cccaacaggc taccacacct tccctggata tccctcctgca 120
ggtcaggagt catcttttcc cccttctggt cagtatcctt atccatagtg ctttccctcca 180
atgggaggag gtgcctaccc acaagtgcc aagtagtggt acccaggagc tggaggctac 240
cctgcgcctg gaggttatcc agcccttga ggctatcctg gtgccccaca gccaggggga 300
gctccatcct atcccgaggc tctccaggc caaggatttg gaggccacc agg tggagca 360
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ccactacctg gtggctttcc tggaggacag atgccttctc agtatcctgg aggacaacct 480
acttacccta gtcagatcaa tacagattct ttttcttct atcctgtttt ctctcctgtt 540
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ccagctgcca acttcgatgc tataagagat gcagaaattc ttcgtaaggc aatgaagggt 660
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aataattttt tagaagggtt ctgaaagctc tgccttccgg aatccctcta agtctgcttg 1920
atagagtgga tagtatgtta aaactgtgta ctttaaaaaa aaattcaacc tttacatcta 1980
gaataatttg catctcattt tgcctaaatt ggttctgtat tcataaacac tttccacata 2040
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ataaaaaatt gcatat 2176

<210> 216
<211> 525
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(525)
<223> 3' terminal sequence. thrombospondin 1
(THBS1) gene.

<400> 216
tcctgnanta nctncaacaa ccgatgtgag ggaaaatcgg tccagacacg gacctgccac 60
attcaggagt gtgacaagag atttaaacag gatggtggct ggagcntgng tccccctgg 120
tcatcttgtt ctgtgacatg tggatgatgt gtgatcacia ggatccggct ctgcaactct 180
cccagccccc agatgaacgg gaaaccctgt gaaggcgaag gcgngagac caaagcctgc 240
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aggaaggta cctacttagg agaaacaaac agaaggcaaa gtccctgcagg ctgagcaact 420
tctttttaat tgaanaacaa attcaccntt tccccagct ttttttcctt gtgttcaggg 480
gaggcagagg ttttttgaac gggnttaggg gatttttgnc aagtt 525

<210> 217
<211> 5722
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(5722)
<223> thrombospondin 1 (THBS1) gene.

<400> 217
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cgccgcgctc cgttacacac aggatccctg ctgggcacca acagctccac catggggctg 120
gcctggggag taggcgtcct gtccctgatg catgtgtgtg gcaccaaccg cattccagag 180
tctggcggag acaacagcgt gtttgacatc tttgaactca ccggggccgc ccgcaagggg 240
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gccaacctga tccccctgt gcctgatgac aagttccaag acctgggtga tgctgtgcgg 360
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ctgctggccc tggagcggaa agaccactct ggccaggtct tcagcgtggg gtccaatggc 480
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gaagaagctc tcttggaac cgccagtggt aagagcatca ccctgtttgt gcaggaagac 600
agggcccagc tgtacatcga ctgtgaaaag atggagaatg ctgagttgga cgtccccatc 660
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143/292

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<210> 218

<211> 397

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(397)

<223> 3' terminal sequence. protein tyrosine
phosphatase, non-receptor type 2 (PTPN2) gene.

<400> 218

ttaatgctgc caaaaagtat aaaaatacag taggaatggc agtacaatac aaagtaatct 60
ctcctaattt atttcttgta catctttcta catttcatac actcattaaa aacacttaac 120
acatccaatt aaagggtctg caaagtcttc tgctgggtgg tgctcttcat ccctgggnt 180
gtaaagttta ctttgtaaac aaacaactgt gaggncaatc tagagggtta ggcgagcctc 240
actttagttt ccggagtggg gcttcagggt cttgctttgc acatcaatgg gttcaaaatt 300
tataggtctg aggaatatc tcaaggatcat ggaatattag gngtctggt ncaat cttgg 360
ggcccttttt tcttttttcg ttncatttct ccattta 397

<210> 219

<211> 338

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(338)

<223> 5' terminal sequence. protein tyrosine
phosphatase, non-receptor type 2 (PTPN2) gene.

<400> 219

ggctccttga accctgacca tgggcctgcg gtgatccact gtagtgcagg cattgggcgc 60
tctggcacct tctctctggt agacacttgt cttgttttga tggaaaaagg agatgatatt 120
aacataaaac aagtgttact gaac atgaga aaataccgaa tgggtcttat tcagacccca 180
gatcaactga gattctcata catggctata atagaaggag caaaatgtat aaaggagat 240

tctagtatac agaaacgatg gaaagaactt tctaaggang acttatctcc tgcctttgat 300
cattncacca aacaaaataa tgactgaaaa atacantg 338

<210> 220
<211> 2287
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2287)
<223> protein tyrosine phosphatase, non -receptor
type 2 (PTPN2) gene.

<400> 220
ggggggcctg agcctctccg ccggcgcagg ctctgctcgc gccagctcgc tcccgcagcc 60
atgccaccca ccctcgagcg ggagttcgaa gagttggata ctacagctcg ctggcagccg 120
ctgtacttgg aaattcgaaa tgagtcccat gactatcctc atagagtggc caagtttcca 180
gaaaacagaa atcgaaacag atacagagat gtaagcccat atgatcacag tctgtgttaa 240
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gtttggcagc agaagaccaa agcagttgtc atgctgaacc gcattgtgga gaaagaatcg 420
gttaaatgtg cagctactg gccaacag at gaccaagaga tgctgtttaa agaaacagga 480
ttcagttgtg agctcttgtc agaagatgtg aagtcgtatt atacagtaca tctactacaa 540
ttagaaaata tcaatagtgg tgaaccaga acaatatctc actttcatta tactacctgg 600
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tgaaaaatct gttactaaaa aaaaaaattg tatgtcgatt gaattgtact ggatacattt 1920
tccatttttt taaaaagaag ttgatatga gcagttagaa gttggaataa g caatttcta 1980
ctatatattg catttctttt atgttttaca gttttcccca ttttaaaaag aaaagcaaac 2040
aaagaaacaa aagtttttcc taaaatatac ttggaaggaa aattctcctt actgggatag 2100
tcaggtaaac agttggtcaa gactttgtaa agaaattggt ttctgtaaat ccattattg 2160
atatgtttat ttttcatgaa aatttc aatg tagttgggtt agattatgat ttaggaagca 2220
aaagtaagaa gcagcatttt atgattcata atttcagttt actagactga agttttgaag 2280
taaacc 2287

<210> 221

<211> 296
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(296)
<223> 3' terminal sequence. epha2 (EPHA2) gene.

<400> 221
ctcggctggc tcacacaccc gtatggcaaa ggggtgggacc tgatgcagaa catcatgaat 60
gacatgccga tctacatgta ctccgtgtgc aacgtgatg t ctggcgacca gganaactgg 120
ctccgcacca actgggtgta ccgaggagag gctgagcgta tcttcattga gctcaagttt 180
actgtacgtg actgcaacag cttccctggg tggcgccant tcttggaag gagactttca 240
acctctacta tgccgagtcg gacctgggac tacggcanca acttncagaa gcgcct 296

<210> 222
<211> 3921
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3921)
<223> epha2 (EPHA2) gene.

<400> 222
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gggtgtgcgg gagccgggct cggggggatc ggaccgagag cgagaagcgc ggcattggagc 120
tccaggcagc ccgcgcctgc ttcgcctctg tctggggctg tgcgctggcc gcggccgcgg 180
cggcgcaggg caaggaagtg gtactgtctg actttgctgc agctggaggg gagctcggct 240
ggctcacaca cccgtatggc aaagggtggg acctgatgca gaacatc atg aatgacatgc 300
cgatctacat gtactccgtg tgcaacgtga tgtctggcga ccaggacaac tggctccgca 360
ccaactgggt gtaccgagga gaggctgagc gtaacaactt tgagctcaac tttactgtac 420
gtgactgcaa cagcttccct ggtggcgcca gctcctgcaa ggagactttc aacctctact 480
atgccgagtc ggacctggac tacgg cacca acttcagaa gcgcctgttc accaagattg 540
acaccattgc gcccgatgag atcacctgca gcagcgactt cgaggcacgc cacgtgaagc 600
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atgtgcgccg caccgagggg ttctccgtga ccct ggacga cctggcccca gacaccacct 1620

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ataagtttct attctgtcag tgttaaagat tttgtttgt tggacatttt tttcgaatct 3840
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agttgcagat gattcaaacc g 3921

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<210> 223

<211> 437

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(437)

<223> 3' terminal sequence. tissue inhibitor of
 metalloproteinase 1 (erythroid potentiating
 activity, collagenase inhibitor) (TIMP1) gene.

<400> 223

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ggaacagggt ggacactgtg caggcttcag ctccactcc gggcaggatt caggctatct 60
gggaccgag gacttgccag gngcacagcc ctggctccc aggcaggcag gcaaggtgac 120
gggactggaa gcccttttca naggcttga ggagctggnc cgtccacaag caatgagtgc 180
cactctgcag tttgcagggt atggataaac agggaaacac tgtgcattcc tcacagcaa 240

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cagtntaggt cttggtnaag ccccggcgct gagctaagct caggcttttc caggggagcc 300
acgaaactnc aggtagtgat gtgcaagagt ccatcctgca gttttccagc aatnagaaac 360
tcctcgttng cgggtttttg ggacnttgg aagtntc cg cagacatttt tccatgggcc 420
gggttttaag acgaacc 437

<210> 224

<211> 466

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(466)

<223> 5' terminal sequence. tissue inhibitor of
metalloproteinase 1 (erythroid potentiating
activity, collagenase inhibitor) (TIMP1) gene.

<400> 224

gccncagatc cagcgccag agagacacca gagaaccac catggccccc ttgnagccc 60
ctggcttctg gcacctgtt g ttgctgtg ctgatagccc ccagcagggc ctgcacctgt 120
gtcccacccc acccacagac ggccttctgc aattccgacc tcgtcatcag ggccaagttc 180
gtggggacac cagaagtcaa ccagaccacc ttataccagc gtatgagat caagatgacc 240
aagatgtata aagggttcca agccttaggg gatgccgctg acatccggtt cgtctacacc 300
cccgccatgg agagtgtctg cggatacttn cacagggtccc acaaccgnag cgaggagt 360
ctcattngct ggaaaactgt aggatggact tctgcacat tnactacctt gcagttttng 420
tgggttcctt gggaacagtc tgagggttag ttnagcggtn ggggtt 466

<210> 225

<211> 782

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(782)

<223> tissue inhibitor of metalloproteinase 1
(erythroid potentiating activity, collagenase
inhibitor) (TIMP1) gene.

<400> 225

aggggcctta gcgtgccgca tcgccgagat ccagcgccca gagagacacc agagaaccca 60
ccatggcccc ctttgagccc ctggcttctg gcacctgtt gttgctgtg ctgatagccc 120
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tcgtcatcag ggccaagttc gtggggacac cagaagtcaa c cagaccacc ttataccagc 240
gtatgagat caagatgacc aagatgtata aagggttcca agccttaggg gatgccgctg 300
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acaaccgcag cgaggagt 420
ctacctgcag tttcgtggct ccctggaaca cctgagctt agctcagcgc cggggcttca 480
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agtccctgcg gtcccagata gctgaatcc tgcgcggagt ggaactgaag cctgcacagt 720
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gc

782

<210> 226
<211> 353
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(353)
<223> 5' terminal sequence. ephrin -a1 (EFNA1)
gene.

<400> 226
acagctacta ctacatctca gccaaaccca tccaccagca tgaagaccgc tgcttgaggt 60
tgaaggtgac tgtcagtggc aaaatcactc acagtcctca ggcccatgac aatccacagg 120
agaagagact tgcagcagat gaccagagg tgcgggttct acatagcatc ggtcacagtg 180
ctgccccacg cctcttccca cttgcctgga ctgtgctgct ccttcactt ctgctgctgc 240
aaaccccgta aaggtgtatg ccacacctgg ccttaaagag ggaca ggctg aagagaggga 300
caggcactcc aaacctgtct tgggggccac ttccagagcc cccagccctt ggg 353

<210> 227
<211> 1480
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1480)
<223> ephrin-a1 (EFNA1) gene.

<400> 227
gcggagaaag ccagtgggaa cccagaccca taggagaccc gcgccccgc tcggcctggc 60
caggccccgc gctatggagt tectctgggc ccctctcttg ggtctgtgct gcagtctggc 120
cgctgctgat cgccacacgg tcttctggaa cagttcaaat cccaagttcc ggaatgagga 180
ctacaccata catgtgcagc tgaatgacta cgtggacatc atctgtccgc actatgaaga 240
tcactctgtg gcagacgctg ccatggagca gtacatactg tacctggtgg agcatgagga 300
gtaccagctg tgccagcccc agtccaagga ccaagtccgc tggcagtga accggcccag 360
tgccaagcat ggcccggaga agctgtctga gaagttccag cgcttcacac ctttcaccct 420
gggcaaggag ttcaaagaag gacacagcta ctactacatc tccaaaccca tccaccagca 480
tgaagaccgc tgcttgaggt tgaaggtgac tgtcagtggc aaaatcactc acagtcctca 540
ggccccatgc aatccacagg agaagagact tgcagcagat gaccagagg tgcgggttct 600
acatagcatc ggtcacagtg ctgccccg cctcttccca cttgcctgga ctgtgctgct 660
ccttcactt ctgctgctgc aaaccccgta aaggtgtatg ccacacctgg ccttaaagag 720
ggacaggctg aagagaggga caggcactcc aaacctgtct tggggccact ttccagagccc 780
ccagccctgg gaaccactcc caccacaggc ataagctatc acctagcagc ctcaaacagg 840
gtcagtatta aggttttcaa ccggaaggag gccaaccagc ccgacagtgc catccccacc 900
ttcacctcgg agggacggag aaagaagtgg agacagtctt tccccaccat tctgccttt 960
aagccaaaga aacaagctgt gcaggcatgg tcccttaagg cacagtggga gctgagctgg 1020
aagggggcac gtggatgggc aaagcttgta aaagatgccc cctccag gag agagccagga 1080
tgcccagatg aactgactga aggaaaagca agaaacagtt tottgcttgg aagccaggta 1140
caggagaggc agcatgcttg ggctgaccca gcattctcca gcaagacctc atctgtggag 1200
ctgccacaga gaagtttgta gccaggctact gcattctctc ccattcctgg gcagcactcc 1260

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ccagagctgt gccagcaggg g ggctgtgcc aacctgttct tagagtgtag ctgtaagggc 1320
agtgcccatg tgtacattct gcctagagt tagcctaaag ggcagggccc acgtgtatag 1380
tatctgtata taagttgctg tgtgtctgtc ctgatttcta caactggagt ttttttatac 1440
aatgttcttt gtctcaaaat aaagcaatgt gttttttcgg 1480
```

<210> 228

<211> 170

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(170)

<223> 3' terminal sequence. endothelin receptor
type a (EDNRA) gene.

<400> 228

```
ttttaaggtt tctgtaaact tttattttac acttatgggc cactgcaact cagggccttg 60
gcttctggct catttctaca agttacttg ttgaaaagat gtagtaaagg tagaaattgg 120
aaatatcct gctagtaaac cacagtact taccagtcca taaataaaat 170
```

<210> 229

<211> 4105

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4105)

<223> endothelin receptor type a (EDNRA) gene.

<400> 229

```
gaattcgcgg ccgcctcttg cgggtcccaga gtggagtgga aggtctggag ctttgggagg 60
agacggggag gacagactg g aggcgtgttc ctccggagtt ttctttttcg tgcgagccct 120
cgcgcgcgcg tacagtcac ccgctggtct gacgattgtg gagaggcggg ggagaggcctt 180
catccatccc acccggtcgt cgccggggat tgggggtccca gcgacacctc cccgggagaa 240
gcagtgccca ggaagttttc tgaagccggg gaagctgtgc agccgaagcc gccgcccgcgc 300
cggagcccgg gacaccggcc accctccgcg ccaccaccc togttttctc cggcttcctc 360
tggtccaggc gccgcgcgga cccggcagct gtctgcgcac gccgagctcc acggtgaaaa 420
aaaaagtga ggtgtaaaag cagcacaagt gcaataagag atatttcctc aaatttgctt 480
caagatggaa accctttgcc tcagggcac cttttggct g gcactgggtg gatgtgtaat 540
cagtgaataa cctgagagat acagcacaaa tctaagcaat catgtggatg atttcaccac 600
ttttcgtggc acagagctca gcttctcgtt taccactcat caaccacta atttggtcct 660
accagcaat ggctcaatgc acaactattg cccacagcag actaaaatta cttcagcttt 720
caaatacatt aacactg tga tatctgtac tattttcatc gtgggaatgg tggggaatgc 780
aactctgtc aggatcattt accagaacaa atgtatgagg aatggcccca acgcgtgat 840
agccagtctt gcccttgagg accttatcta tgtggtcatt gatctcccta tcaatgtatt 900
taagctgctg gctgggcgct ggcttttga tcacaatgac tttggcgat ttctttgca a 960
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tagtgttgac aggtacagag cagttgcctc ctggagtcgt gttcagggaa ttgggattcc 1080
tttgtaact gccattgaaa ttgtctccat ctggatcctg tcctttatcc tggccattcc 1140
tgaagcgatt ggctcgtca tggtaacctt tgaa tatagg ggtgaacagc ataaaacctg 1200
tatgtcfaat gccacatcaa aattcatgga gttctaccaa gatgtaaagg actggtggct 1260
```

```

cttcgggttc tatttctgta tgcccttgggt gtgcactgcg atcttctaca cctcatgac 1320
ttgtgagatg ttgaacagaa ggaatggcag cttgagaatt gccctcagtg aacatcttaa 1380
gcagcgtcga gaagtggcaa aaacagtttt ctgcttgggt gtaatttttg ctctttgctg 1440
gttccctctt cacttaagcc gtataattgaa gaaaactgtg tataacgaaa tggacaagaa 1500
cogatgtgaa ttacttagtt tcttactgct catggattac atcgggtatta acttggcaac 1560
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catgaacgga acaagcatcc agtgggaagaa ccacgatcaa aacaaccaca acacagaccg 1740
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aatcctctcg gagaaaaaaa tc acaaggca actgtgactc cgggaatctc ttctctgatc 1860
cttcttctct aattcactcc cacaccaag aagaaatgct ttccaaaacc gcaaggtaga 1920
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aatgaaaacc agaaggatat ttactacttt tgcatgaaaa tagagctttc aagtacatgg 2100
ctagctttta tggcagttct ggtgaatgtt caatgggaac tggtcacccat gaaactttag 2160
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taatagccta acatgattat ttgaacttat ttacacatag ttgaaaaaa aaaagacaaa 2340
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atggtgtttt attacaaggg acctgaaca tgttttgat gttaaattca aaagtaatgc 2580
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atgattcgga aattttcatt caggtatttg taatagtac atatatatgt atatacatat 2820
cacctcctat tctcttaatt tttgttaaaa tgttaactgg cagtaagtct tttttgatca 2880
ttcccttttc catataggaa acat aatttt gaagtggcca gatgagtta tcatgtcagt 2940
gaaaaataat taccacaaa tgccaccagt aacttaacga ttcttcaact cttgggggtt 3000
tcagtatgaa cctaactccc caccocaaca tctccctccc acattgtcac catttcaaag 3060
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gtctgagcta aaatctaggt gattgttcat catgacaa cc tgcctcagtc cattttaacc 3360
tgtagcaacc ttctgcattc ataaatcttg taatcatgtt accattacaa atgggatata 3420
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tggtttgata aagcagtatt tggggtcata ttgtttcctg tgctggagca aaagtcatta 3540
cactttgaag tatttatatt ttcttatcct caattcaatg tggatgaa attgccaggt 3600
tgtctgatat ttctttcaga cttcgccaga cagattgctg ataataaatt aggtgaagata 3660
atttgttggg ccatatttta ggacaggtaa aataacatca ggttcagtt gcttgaattg 3720
caaggctaag aagtactgcc cttttgtgtg ttagcagtc aatctattat t ccaactggcg 3780
catcatatgc agtgatatat gcctataata taagccatag gttcacacca tttgttttag 3840
acaattgtct ttttttcaag atgctttgtt tctttcatat gaaaaaaatg cattttataa 3900
attcagaaag tcatagattt ctgaaggcgt caacgtgcat tttatttatg gactggtaag 3960
taactgtggt ttactagcag gaatat ttcc aatttctacc ttactacat cttttcaaca 4020
agtaactttg tagaaatgag ccagaagcca aggcctgag ttggcagtg cccataagt 4080
taaaataaaa gtttacagaa acctt 4105

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<210> 230

<211> 240

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(240)

<223> 3' terminal sequence. growth factor
receptor-bound protein 2 (GRB2) gene.

<400> 230

ggtttcttgt tttttattat tggcgtcagt agngactata cgtggcctta aacgtcatgc 60
actgatggac agaagagaaa aaaggatgaa aaaaaagaca aaggagggga aagaggagca 120
gcagtgaan tttgtaataa aaactcttct taatttatag gtaagttttg gcatttttaa 180
atccaacgac ccctcccacc ccctaaagt ccaaccaaag tgagaggggc acagggtgac 240

<210> 231

<211> 475

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(475)

<223> 5' terminal sequence. growth factor
receptor-bound protein 2 (GRB2) gene.

<400> 231

cttaatggaa aagacggctt cattcccaag aactacatag aaatga aacc acatccgtgg 60
ttttttggca aaatccccag agccaaggca gaagaaatgc ttagcaaaca ggggcacgat 120
ggggcctttc ttatccgaga gagtgagagc gtccttgggg acttctccct ctctgtcaag 180
tttgaaaacg atgtgcagca cttcaagggtg ctccgagatg gagccgggaa gtacttcctc 240
tgggtggtga agttcaattc tttga atgag ctggtggatt atcacagatc tacatctgtc 300
tcagaaaacc agcagatatt cctgcgggga cattaggaac aggtgccaca gcaggccgac 360
atacgttcca ggggcctttt tttgattttt gattccccag gggggnttgg ngagggtggg 420
ttttccgccg ggggagattt tattccatgt tcntgggtn aatttaggaa ccntt 475

<210> 232

<211> 1109

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1109)

<223> growth factor receptor -bound protein 2
(GRB2) gene.

<400> 232

gccagtgaat tcgggggctc agccctcctc cctcccttcc ccctgcttca ggctgctgag 60
cactgagcag cgctcagaat ggaagccatc gccaaatatg acttcaaagc tactgcagac 120
gacgagctga gcttcaaaaag gggggacatc ctcaagggtt tgaacgaaga atgtgatcag 180
aactggtaca aggcagagct taatggaaaa gacggcttca ttccaagaa ctacatagaa 2 40
atgaaaccac atccgtggtt ttttggcaaa atccccagag ccaaggcaga agaaatgctt 300
agcaaacagc ggcacgatgg ggcctttctt atccgagaga gtgagagcgc tcctggggac 360
ttctccctct ctgtcaagtt tggaaacgat gtgcagcact tcaagggtgct ccgagatgga 420
gccgggaagt acttctctctg ggtggtgaag ttcaattctt tgaatgagct ggtggattat 480
cacagatcta catctgtctc cagaaaccag cagatattcc tgcgggacat agaacagggtg 540
ccacagcagc cgacatacgt ccaggccctc tttgactttg atccccagga ggatggagag 600
ctgggcttcc gccggggaga ttttatccat gtcatggata actcagaccc caactggtgg 660


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aaaggagctt gccacggg ca gaccggcatg tttccccgca attatgtcac ccccgtagac 720
cggaacgtct aagagtcaag aagcaattat ttaaagaaag tgaaaaatgt aaaacacata 780
caaaagaatt aaaccacaa gctgcctctg acagcagcct gtgagggagt gcagaacacc 840
tggccgggtc accctgtgac cctctcactt tgggttgaac tttagggggg gggagggggc 900
gttgatttta aaaatgccaa aacttaccta taaattaaga agagttttta ttacaaattt 960
tactgtctgc tcctctttcc cctcctttgt cttttttttc atcctttttt ctcttctgtc 1020
catcagtga tgacgtttta ggccacgtat agtcctagct gacgccaata ataaaaaaca 1080
agaaaccaa aaaaaaaac ccgaattca 1109
```

<210> 233

<211> 446

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(446)

<223> 3' terminal sequence. jun d proto -oncogene
(JUND) gene.

<400> 233

```
cgcgctctc ggctgccnng ntgtacaccg cgccggaaag tggggctcgc agggggcgca 60
ctcaaaaccc tgccttttct ttactttttac tttttttttt ttttctttgg aagagagaag 120
aacagagtgt tcgattctgc cctattttatg tttctactcg ggaacaaacg ttggttgtgt 180
gtgtgtgtgt tttcttgtgt tggtttttta a agaaatggg aagaagaaaa aaaaattctc 240
cgcccccttc ctgatctcgc ctccccctt cggttctttc gaccgggtcc cccctccctt 300
ttttgtttct gttttgtttt gttttgctac gagtccacat tctgtttgt aatccttggg 360
ttcgnccggg tttctgtttt cagtaaagtc tcgttacggc aaaacctcgt gccgaatttt 420
tggggctcga ggggcaaaat ttccca 446
```

<210> 234

<211> 1891

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1891)

<223> jun d proto -oncogene (JUND) gene.

<400> 234

```
ccgaggctat aagagggcgc acaagtggcg cggcgcagga gccgcgccca gtggagggcc 60
gggcgtctcg gccgcggccg gggcgggcgc agggccgagc ggacgggggg gcgcggggcc 120
cccgggaggg cgcgccact cccccccggg ccggcgcggc gggggagggc gaggatggaa 180
acacccttct acggcgatga ggcgctg agc ggctggggcg gcggcgccag tggcagcggc 240
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agcatgatga agaaggacgc gctgacgctg agcctgagt agcaggtggc ggcagcgctc 360
aagcctgcgc ccgcgccgcg ctctacccc cctgccgcgc acggcgcccc cagcgcgcca 420
ccccccgacg gctgtctcgc ctctcccgac ctggggctgc tgaagctggc ctcccccgag 480
ctcagcgccc tcatcatcca gtccaacggg ctggtcacca ccacgccgac gagctcacag 540
ttctctacc ccaaggtggc ggccagcgag gaggcaggat tcgccgaggg ctctgtcaag 600
gccctggagg atttacacaa gcagaaccag ctggcgcgcg gccgggc cgc tgcgcgcgcc 660
gccgcgcgcg ccggggggcc ctggggcacg gccacgggct ccgcgcccc cgcgagctg 720
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153/292

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gccccggcgg cgcccgcgcc cgaagcgcc gtctacgca acctgagcag ctacgcgggc 780
ggcgccgggg ggcgggggg cgcccgacg gtcgccttcg ctgccgaacc tgtgcccttc 840
ccgcccgcgc cccccccagg cgcgt tgggg ccgcccgcgc tggctgcgct caaggacgag 900
ccacagacgg tgcccacgt gccgagcttc ggcgagagcc cgccgttgct gcccatcgac 960
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cagggtcccg cgtactgagt cgggcattgc ggccacctcc aaggggcggg ctgcgggggg 1260
ggtgtcgtgg gcgcccggga cttggagagg gtgcggccct ccaccccccc ctccccgagt 1320
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gcgtctcgcc tgccccttg tacaccgcgc cgcaaggggg ctccgagggg gcgcacgtca 1560
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gttcgattct gccctattta tgtttctact cggggaacaa acgttggtg tgtgtgtgtg 1680
tgtttctttg tgttggttt ttaaagaaat gggaagaaga aaaaaaatt ctcc gccct 1740
ttcctcgatc tcgctcccc ttcggtcttt cgaccgtccc cccctcccct tttttgttc 1800
tgttttgttt tgttttgcta cgagtccaca ttctgtttg taatccttg ttcgcccgt 1860
tttctgttt cagtaaagtc tcgttacgcc a
1891

```

<210> 235

<211> 421

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(421)

<223> 3' terminal sequence. swi/snf related,
matrix associated, actin dependent regulator of
chromatin, subfamily a, member 2 (SMARCA2) gene.

<400> 235

```

accaaaagtc ttcaagccac gagcggaggg cattcctgca ggccatcttg gagcatgagg 60
aggaaaatga ggaagaagat gaagtaccgg acgatgagac tctgaaccaa atgattgctc 120
gacgagaaga agaatttgac ctttttatgc ggatggacat ggaccggcgg agggaagatg 180
cccggaaccc gaaacggaag ccccgtttaa tggaggagga tgagctgcc tctggntca 240
ttaaggatga cgctgaagta gaaaggctca cctgtgaaga agaggaggag aaaatatttg 300
ggaggggggc ccgccagcgc cgtgacgtgg actacagtga cgccctcacg gagaagcagt 360
ggctaaaggg cntcgaaga cggcatttng gaggaattng aagaggaata c ggttaagaa 420
g
421

```

<210> 236

<211> 438

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(438)

<223> 5' terminal sequence. swi/snf related,
matrix associated, actin dependent regulator of

chromatin, subfamily a, member 2 (SMARCA2) gene.

<400> 236

```

tggcaatttt ctgccgggca ctcttaaaca ctgactgtaa gacgatggag tttcataga 60
tctgggatcc ctccaggttg aacgtctgag cg ttgtgaca gagaagcatg acatccttct 120
ccaggctgcc taggctccgg tacttatgat tacgaatcct ttccctttatt tttttgaaat 180
ccactggctt cctaattaat tcatagtatt ctggtaattc ttcccttgaa ggtaactgaa 240
tgaagacttc actgagctgt cgccctgaac tgtttccttc tatttccaac tgagaattac 300
tgggcacctt ctccacgtta cacctatctt tgtagtttat cacagtattc gatgattagc 360
gttcatctgg ctttgtcagt ttggggggga tttggtgaca gntttntcag cgggagggcg 420
gcctcttctc ttcttagg                                     438

```

<210> 237

<211> 5257

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5257)

<223> swi/snf related, matrix associated, actin
dependent regulator of chromatin, subfamily a,
member 2 (SMARCA2) gene.

<400> 237

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aaaaattttc tgttaccaaa ttttacaact tctaataaga ctactataac tttatgtaaa 60
ctgatgaaga tgtgctgatt aacatattct gtgatatggt ttacaacttt taatcataat 120
tgtccatgat tttggaatgc tgttatattat cagtaaatgt aaaatatttg aggcathtag 180
ccatacacac actagaactt tttaaaactt tgtcctatag tgtaatta ta aactgatgac 240
tattatcttc atacattgag ttttcatgca tcaatgaaat gaaaaatata ggagtagatg 300
tccacgcccc cagaccctgg tgcgatgcc caccagggc cttcgccggg gcctgggcct 360
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agcatgatgg ggccaagtcc tggacc tcca agtgtctccc atcctatgcc gacgatgggg 480
tccacagact tccacagga aggcattgat caaatgcata agcccatcga tggatatacat 540
gacaagggga ttgtagaaga catccattgt ggatccatga agggcactgg tatgcgacca 600
cctcaccag gcattggccc tcccagagt ccaatggatc aacacagcca aggttatatg 660
tcaccacac catctccatt aggagcccc gagcacgtct ccagccctat gtctggagga 720
ggcccaactc cactcagat gccaccaagc cagccggggg cctcatccc aggtgatccg 780
caggccatga gccagcccaa cagaggtccc tcacctttca gtctgtcca gctgcatcag 840
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cagccgccgc aaccacagac gcagcaacaa cagcagccgg cccttggtta ctacaacaga 1080
ccatctggcc cggggccgga gc tgagcggc ccgagcacc cgcagaagct gccggtgcc 1140
gcgcccggcg gccggccctc gccgcgccc cccgcagccg cgcagccgcc cgcggccgca 1200
gtgcccgggc cctcagtgc gcagccggcc ccggggcagc cctcgccctg cctccagctg 1260
cagcagaagc agagccgcat cagccccatc cagaaaccgc aaggcctgga ccccggtgaa 1 320
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agaatcgccg gactgatggc tgaagatgag gagagttata gaaaactgat tgatcaaaag 1860
aaagacaggc gtttagctta ctttttgag cagaccgatg agtatgtagc caatctgacc 1920

```

```

aatctggttt gggagcacia gcaagcccag gcagccaaag agaagaagaa gaggaggagg 1980
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gagcccatag atgagagcag ccagatgagt gacctccctg tcaaagtac tcacacagaa 2100
accggcaagg ttctgttcgg accagaagca cccaaagcaa gtcagctgga cgctggctg 2160
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gcactgggtt gtttctatat catcatcgtc tataaactag ctttaggata gtgccagaca 5160
aacatatgat atcatggtgt aaaaaacaca cacatacaca aatatttgtg accaa atggg 5220
cctcaaaagat tcagattgaa acaaacaaaa agctttt 5257

```

<210> 238

<211> 507

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(507)

<223> 3' terminal sequence. protein phosphatase 2
(formerly 2a), regulatory subunit b (pr 52), gamma
isoform (PPP2R2C) gene.

<400> 238

```
tacatgctca cccgggacta ccttacagtc tatggatggg acctgaacat ggaggcaaga 60
cccatagaga cctaccaggt ccatgactac cttcggagca agctctgttc cctgtacgag 120
aacgactgca ttttcgacaa gtttgaatgt gcctggaacg ggagcgacan tncatcatga 180
ccggggccta caacaacttc ttccgcatgt tcgatcggaa caccaagcgg gacgtgaccc 240
tgaggagcct cgagggaag cagcaagccc cgggctgtgc tcaagccacg gcgcgtgtgc 300
gtgggggggc aagcgcgggc gtgnatga ca tcagtgtggg acagcttggg acttcaccaa 360
gaagatcctg cacacggcct ggcacccggc tgaggaacat catttgccat tcgccgccac 420
caacaacctg ttacatcttt ccaggggcaa ggtaaatttt tgacattgca ttaggtattn 480
tgcaatttcc cggnccttgc caaccca 507
```

<210> 239

<211> 521

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(521)

<223> 5' terminal sequence. protein phosphatase 2
(formerly 2a), regulatory subunit b (pr 52), gamma a
isoform (PPP2R2C) gene.

<400> 239

```
taaacagaca attactgcca aacacaattc tggcctagga aagcggggnn gggagggggc 60
ccaaacttcc tgtgtccaca cactgccacc tctgcagctg tcctcatcag tgggtgtgact 120
ttcttcccct ccttgcatgt cggtcgtgaa ggtcatgtcg gggatgactt gcatgaggct 180
gggtggcagg ggccgggaac tgcacatacc tagtgcattg cagagtttac cttgtcctgg 240
aagatgtaca ggttggttgg ggcggcgatg gcaatgatgt tctcagccgg gtgccaggcc 300
gtgtgcagga tcttcttggg gaagtccaag ctgttccaaa atgatgtcat cacgccggcc 360
cttgccccc acgnaaangg ncnnttggtt tnagcaaagc ccng ggtttg ttgcttttcc 420
ctngnaggcn tncaggntca agtnccnttt ggtnttnc cc gatcgaacat ncggaagaat 480
tttttttagg ccccntcat gatgaacgtg tncgttccct t 521
```

<210> 240

<211> 350

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(350)

<223> 3' terminal sequence. thrombospondin 3
(THBS3) gene.

<400> 240

```
cagattcatt nnnnganntg cctgtgacaa ttgccccaac gttccaaca atgaccagaa 60
ggacacagat ggcaatgggg aaggagatgc ctgtgacaac gac gtggatg gggatggtgc 120
aggcctgggg ctgaagggtt ggctggggga cctgtgagaa ttggatcag gtggggatga 180
agcagggaag ctaggaagtc tctgtgaaat agggaggcag gcttntggac gttggcctgg 240
gtgaggagag attacctgca gcagatgtca ataggaatnt gaggtagggc gtagtnttag 300
gcagagtttg gactagaggg t nagacaaga aacaggcaga tttcctggcc 350
```

<210> 241

<211> 2871

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2871)

<223> thrombospondin 3 (THBS3) gene.

<400> 241

```
atggagacgc aggaacttcg gggggccctg gctcttctcc tcctttgctt tttcacatct 60
gccagtcagg atctgcaggt aattgacctg ctgactgtgg gcgagtctcg gcagatggta 120
gctgtggcag agaagatccg gacagccttg ctcactgctg gggacatcta cctcttatcc 180
accttccgcc tgcccccaa gcagggtggt gtctcttttg g cctctattc tcgccaagac 240
aacactcgat ggctggaggc ctctgttgta ggcaagatca acaaagtact ggtgcgatac 300
cagcgggagg atggcaaaagt ccacgccgtg aacctacagc aagcgggcct ggctgatggg 360
cgcacacaca cagttctcct gcgactccga ggtccctcca gaccagccc tgccctacat 420
ctctacgtgg actgcaaaact gggtgaccaaa catgcaggcc ttccagcaat ggccccatt 480
ctccacgcgg aggtcgatgg gctggagatt aggactggac agaaggcgta tttgaggatg 540
cagggccttg tggaatctat gaaaattatt ctgggtgggt ccatggcccg ggtaggagcc 600
ctgagtgagt gtccattcca aggggacgag tccatccaca gtgcagtgc caatgcactg 6 60
cactccattc taggggagca gaccaaggcg ctggtcacc aactcaccct cttcaaccag 720
atcctggttg agctgcggga tgatatacga gaccaggtaa aggaaatgtc cctgatccga 780
aacaccatta tggagtgtca ggtgtgcggc ttccatgagc agcgttccca ctgcagcccc 840
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cgctgggtt tctgggcaa ccagagccag ggctgcctcc cagcccggac ctgccacagc 1260
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ctgttcccca acaaagacca gcagaactca gatacagatt catlttggtg tgcctgtgac 1620
aattgcccc aagttcccaa caatgaccag aaggacacag atggcaatgg ggaaggagat 1680
gcctgtgaca acgactgga tggggatggc atccccaatg gattggacaa ttgccctaaa 1740
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tgtgatacta atgaagacag cgatggggat gggcatcagg acaccaagga caactgccc 1920
cagctgcaa atagctcca gctggactct gataacgatg gac ttggaga tgagtgtgat 1980
ggggatgatg acaatgatgg catcccagat tatgtgcctc ctggtcccg taactgccgc 2040
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ctggtaccca atcccaatca gaaggactca gatggcaatg gcgttggtga tgtgtgtgag 2100
gatgactttg acaatgatgc tgtggtcgac cccctggatg tgtgtcctga aagtgcagag 2160
gtaacgctta cggatttt cg gccctatcag accgtcgtcc tggatcctga gggatgatgct 2220
cagattgacc caaactgggt tgtgtcctcaac cagggcatgg aaatcgttca gaccatgaac 2280
agtgaccctg gcttggcagt tggatacacg gccttcaatg gtgtggactt tgaaggcacc 2340
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tgcttctccc aagaaaacat aatttggtcc aatctccagt atcgatgcaa tgacacagt 2820
cctgaggact ttgagccatt ccggaggcag ctgctccagg gaagggtgtg a 2871

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<210> 242

<211> 509

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(509)

<223> 3' terminal sequence. actin, gamma 1 (ACTG1) gene.

<400> 242

```

cacttttatt ttnccttaca caatgacgtg ttgctggggc ctaatgtntc cacataacag 60
tagaaaaacca aaatttggtg tcatctcttc aaagantcga ganttgcgta caaaaaaac 120
cttacataan ttaagantga ntacatttac aggcgtaaat gcaaaccgnt tccaactcaa 180
agcaagtaac agcccacggt gttctggcca aagacatcag ctaagaaagg aaactggggn 240
cctacggctt gggactttcc aacctggac aggaccgca agncaaac aactgggttc 300
ttgccagcct ctaggaggaa ttcccggaac actcaggccc tggacangtt taataccagg 360
ggggancagt taactttcan tacaggggnc aaaatcaggc aacagttt tt accantccag 420
tggctgggtt cnggttacag gtttcagggg catthtnttt tcggaggggt tnttcccggt 480
tcgtgagggt aggtgagggt tttntgctt 509

```

<210> 243

<211> 393

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(393)

<223> 5' terminal sequence. actin, gamma 1 (ACTG1) gene.

<400> 243

```

gatcacggcc ctggccccag caccatgaag atcaagatca tcgcaccccc agagcgcaag 60
tactcgggtg ggatcgggtg ctccatcctg gcctcactgt ccaccttc a gcagatgtgg 120
attagcaagc aggagtacga cgagtcgggc cctccatcg tccaccgcaa atgcttctaa 180
acggactcag cagatgcgta gatthtctg catgggttaa ttgagaatag aaatttgccc 240

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ctgggaaatt gcacacacct catgctagcc tcacgaaact gggaataagc ctttcgaaaa 300
gaaattgtcc ttgaagcttg tatctgg tat cagcactggg ntgttaggaa nttgttgctg 360
atttttgacc ttgtanttga agtttaactg ttt 393

<210> 244

<211> 1919

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1919)

<223> actin, gamma 1 (ACTG1) gene.

<400> 244

gtctcagtcg ccgctgccag ctctcgact ctgttcttcc gccgctccgc cgtcgcgttt 60
ctctgccggt cgcaatggaa gaagagatcg ccgcgctggt cattgacaat ggctccggca 120
tgtgcaaagc tgggttttgc tgggacgacg ctcccgcgag cgtgtttcc t tccatcgctg 180
ggcgccccag acaccagggc gtcatggtgg gcatgggcca gaaggactcc tacgtgggcg 240
acgaggccca gagcaagcgt ggcatcctga ccctgaagta cccattgag catggcatcg 300
tcaccaactg ggacgacatg gagaagatct ggcaccacac cttctacaac gagctgcgcg 360
tggccccgga ggagcaccca gtgctgc tga ccgaggcccc cctgaacccc aaggccaaca 420
gagagaagat gactcagatt atgtttgaga ccttcaacac cccggccatg tacgtggcca 480
tccaggccgt gctgtccctc tacgcctctg ggcgcaccac tggcattgtc atggactctg 540
gagacggggt caccacacag gtgcccatct acgagggcta cgccctccc cagccatcc 600
tgcgtctgga cctggctggc cgggacctga ccgactacct catgaagatc ctcactgagc 660
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tgtgtacgt cgccctggac ttcgagcagg agatggccac cgccgcaccc tcctcttctc 780
tggagaagag ctacgagctg cccgatggcc aggtcatcac cattggc aat gagcggttcc 840
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cgcaattctc gattctttga agagatgaca acaaattttg gttttctact gttatgtgag 1860
aacattaggc cccagcaaca cgtcattgtg taaggaaaaa taaaagtgc g ccgtaacc 1919

<210> 245

<211> 467

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

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<220>
<221> misc_feature
<222> (1)..(467)
<223> 3' terminal sequence. integrin, alpha 6
(ITGA6) gene.

<400> 245
ccgcgcgcgg gcagctgtgc ttgctctacc tgtcggcggg gctcctgtcc cggctcggcg 60
cacttncaac ttggacactc gggaggacaa cgtgatccgg aaatatggag accccgggag 120
cctcttcggc ttctcgctgg ccactgcactg gcaactgcag cccgaggaca agcggctgtt 180
gctcgtgggg gcccgcggg agnaagcgt tccactgcag agagccaac a gaacgggagg 240
gctgtacagc ttgcgacatc accgcccggg ggccatgcac ggggatcgag tttnataacg 300
atgcttgacc ccacgtcaga aagcaaggaa gattagtgg atngggggtc aacgtccaga 360
gccaaaggttc agggggcaag gtctgtgacat gtgttnaccc tattgaaaaa aggcagcntt 420
ttattacgna gcangatttc cgagaca ttt ttgggcggtt tttttcc 467

<210> 246
<211> 473
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(473)
<223> 5' terminal sequence. integrin, alpha 6
(ITGA6) gene.

<400> 246
gccctctccc atccatatcg tcttcaatcc tgagattctg actcaggaca naacaccgcc 60
caaagatgtc tcgggattcc tgcttcgtat taacatgctg ccttttttca tatcggtgag 120
cacatgtcac gaccttgccc cctggacctt ggctctggac ggtgaccccc atccactgat 180
cttccttgct ttctgacgtg gggtc agcat cgttatcaaa ctcgatccgc gtgcattggc 240
cccgggcggt ggatgtcgca gctgtacagc cctcccgttc tgttggtct ctgcagtggg 300
aagcgttctt gcccgcggg cccccacgga gcaacagccg cttgtcctcg ggctgcagtt 360
gccagtgcag gggccagcga gaaagccgaa gaggttcccc ggggtnttcc atattttccg 420
gatcaagttg ttcctnccga gttttccaag ttgaagggt tgcgcaaggc cgt 473

<210> 247
<211> 5611
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(5611)
<223> integrin, alpha 6 (IT GA6) gene.

<400> 247
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<210> 248

<211> 406

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(406)

<223> 3' terminal sequence. rad9 (s. pombe)
homolog (RAD9) gene.

<400> 248

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cgntgctatt gattcattaa aaaaagaaaa gaaaaa taca ccaaggttcc atntcccccg 240
tgacaggtgg gcctnagggg tcggggtnac cccccccag natggcagca tgattntnt 300
acaatcaatc catcatnttg ggcacagggt ggttttcggg ggctattntt tggctttggc 360
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<210> 249

<211> 2102

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2102)

<223> rad9 (s. pombe) homolog (RAD9) gene.

<400> 249

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at 2102
```

<210> 250

<211> 365

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(365)

<223> 3' terminal sequence. activating
transcription factor 3 (ATF3) gene.

<400> 250

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tacagaaaat tgtaatgata ccattgagta caattaaaca ctctgagaat ttcacagaaa 120
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<210> 251

<211> 453

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(453)

<223> 5' terminal sequence. activating
transcription factor 3 (ATF3) gene.

<400> 251

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gcaacggcca gggttgtgct ttctagcaaa tatgctgt ta tgtccagaaa ttgtgtgtgc 120
aagaaaacta ggcaatgtac tcttcogatg tttgtgtcac acaacactga tgtgactttt 180
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<210> 252

<211> 2056

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2056)

<223> activating transcription factor 3 (ATF3)
gene.

<400> 252

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aagcagcatt tga tatacat gctcaacctt catcggccca cgtgtattgt ccgggtcag 780

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<210> 253

<211> 502

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(502)

<223> 3' terminal sequence. v-akt murine thymoma
viral oncogene homolog 2 (AKT2) gene.

<400> 253

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<210> 254

<211> 1715

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1715)

<223> v-akt murine thymoma viral oncogene homolog
2 (AKT2) gene.

<400> 254

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ccccggagta cctggcgctt gaggtgctgg aggacaatga ctatggcgg gccgtggact 1200
ggtgggggct ggggtgtggtc atgtacgaga tgatgtgagg ccgcctgccc ttctacaacc 1260
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tcagccccga ggccaagtcc ctgcttgctg ggctgcttaa gaaggacccc aagcagaggc 1380
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actggcagga cgtggtccag aagaagctcc tgccaccctt caaacctcag gtcacgtccg 1500
aggtcagac aaggtacttc gatgatgaat ttaccgcccc gtocatcaca atcacacccc 1560
ctgaccgcta tgacagcctg ggctt actgg agctggacca gcggacccac ttccccagt 1620
tctctactc ggccagcatc cgcgagtgg cagtctgcc acgcagagga cgcacgctcg 1680
ctgccatcac cgctgggtgg ttttttacc ctgcc 1715

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<210> 255

<211> 431

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(431)

<223> 5' terminal sequence. s100 calcium-binding
protein, beta (neural) (S100B) gene.

<400> 255

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gagaggatgt ctgagctgga gaaggccatg gtggcctcat cgacgttttc caccaatatt 60
ctggaaggga gggagacaag cacaagctga agaaatccga actcaaggag ctcatcaaca 120
atgagctttc ccatttctta gaggaatca aagagcagga ggttgtggac aaagtcatgg 180
aaacactgga caatgatgga gacggcgaat gtgacttcca gggaattcat ggcctttgtt 240
gccatggtta ctactgcctg ccacgagttc ttggaacat g agtnagatta ggaaagcagc 300
caaacctttt cctgttaaca gaggacggtt catggcaaga naggcaggac aggcaagggg 360
tttgacggct tagttaggga gcttgagggt tttccagccg tntttnttg gtttaatttag 420
ggaaggtttg a 431

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<210> 256

167/292

<211> 1095
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1095)
<223> s100 calcium-binding protein, beta (neural)
(S100B) gene.

<400> 256
tgccgcccag gaccgcgacg agagacg acg cctgcagcaa ggagaccagg aaggggtgag 60
acaaggaaga ggaatgtctga gctggagaag gccatggtgg ccctcatcga cgttttccac 120
caatatctctg gaagggaggg agacaagcac aagctgaaga aatccgaact caaggagctc 180
atcaacaatg agctttccca tttcttagag gaaatcaaag agcaggaggt tgtggacaaa 240
gtcatggaaa cactggacaa tgatggagac ggcgaaatgtg acttccagga attcatggcc 300
tttgttgcca tggttactac tgccctgccac gagttctttg aacatgagtg agattagaaa 360
gcagccaaac ctttccctgta acagagacgg tcatgcaaga aagcagacag caagggcttg 420
cagcctagta ggagctgagc tttccagccg tgtttagctg aattagga ag cttgatttgc 480
tttgtgattg aaaaattgaa aacctctttc caaaggctgt ttttaacggcc tgcattcattc 540
tttctgctat attaggcctg tgtgtaagct gactggcccc agggactctt gttaacagta 600
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tgcgcttcctc atccatgcag ataacagctg gttggccggt gtggccctgc aagggcggtg 840
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cgtcctggaa aaagcaactc catcagaact cgcaatccga gccagctctg ggggctccag 960
cgtggcctcc gtgacccatg cgattcaagt cgcggtgca ggatccttgc ctccaacgtg 1020
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gcgttcaata aaaag 1095

<210> 257
<211> 542
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(542)
<223> 3' terminal sequence. atp-binding cassette,
sub-family b (mdr/tap), member 1 (ABCB1) gene.

<400> 257
ttttaaaatc tactttaatt ctgttataaa atttataatg cagtttaaac tatgatttct 60
ctccacttga tgatgtctct cactctgttc ctttaattac gaagtctctg aagactctga 120
acttgactga ggaaatgtta aacagatacc tcttcataat tctgtaagtgt ttgtctttta 180
actttgaata aatgtcatat ctaaacaat attaaaaagt atttaacatc tcatacagtc 240
agagttcact ggcgctttgt tccagcctgg acactgacca ttgaaaaata gatgcctttc 300
tgtgccagca gctgctgatg cgtgccatgc tcttgactc tgccattctg aaacaccact 360
attaagtctg cattctggat ggtggacagg cggtagcaa tcacaatgca ggtgcggcct 420
tctctggcta tgccagggtc tcttgacaa ctttttcacc tactgtatcc agagctgacg 480
tggtctatcc aaaagcaaaa tantgggctg tctaacaagg gcacgagcta ttgcatgagc 540
tt 542

<210> 258
<211> 4643
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(4643)
<223> atp-binding cassette, sub-family b
(mdr/tap), member 1 (ABCB1) gene.

<400> 258
cctactctat tcagatattc tccagatt cc taaagattag agatcatttc tcattctcct 60
aggagtactc acttcaggaa gcaaccagat aaaagagagg tgcaacggaa gccagaacat 120
tcctcctgga aattcaacct gtttcgcagt ttctcgagga atcagcattc agtcaatccg 180
ggccgggagc agtcatctgt ggtgaggctg attggctggg caggaaacagc gccggggcgt 240
gggctgagca cagcgcttgc ctctctttgc cacaggaagc ctgagctcat tcgagtagcg 300
gctcttccaa gctcaaaagaa gcagaggccg ctgttcgttt ccttttaggtc ttccactaa 360
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cgggatggat cttgaagggg accgcaatgg aggagcaaag aagaagaac t tttttaact 480
gaacaataaa agtgaaaaag ataagaagga aaagaaacca actgtcagtg tattttcaat 540
gtttcgctat tcaaattggc ttgacaagtt gtatatggtg gtgggaactt tggctgccat 600
catccatggg gctggacttc ctctcatgat gctggtgttt ggagaaatga cagatatctt 660
tgcaaatgca ggaaatttag aagatct gat gtcaaacatc actaatagaa gtgatatcaa 720
tgatacaggg ttcttcatga atctggagga agacatgacc aggtatgcct attattacag 780
tggaattggt gctggggtgc tgggtgctgc ttacattcag gtttcatttt ggtgcctggc 840
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ctccaagatt aatgaaggaa ttggtgacaa aattggaatg ttctttcagt caatggcaac 1020
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ggccatcagt cctgttcttg gactgtcagc tgcgtctgg gcaaa gatac tatcttcatt 1140
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agcaattaga actgtgattg catttgagg acaaaagaaa gaacttgaaa ggtacaacaa 1260
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agcagcttat gaaatcttca agataattga taataagcca agtattgaca gctattcga a 1560
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tgagaaagct gtcaaggaag ccaatgccta tgaactttatc atgaaactgc ctcataaatt 1980
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aaatggaggc ctgcaaccag catttgcaat aatattttca aagattatag gggtttttac 2640
aagaattgat gatcctgaaa caaaacgaca gaatagtaac ttgttttcac tattgtttct 2700

agcccttga attatttctt ttattacatt ttctcttcag ggtttcacat ttggcaaagc 2760
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tgtgagttgg tttgatgacc ctaaaaacac cactg gagca ttgactacca ggctcgccaa 2880
tgatgctgct caagttaaag gggtataggt ttccaggctt gctgtaatta cccagaatat 2940
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tgctcagagt ttgcaggtag catacagaaa ctctttgagg aaagcacaca tctttggaat 3240
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caagtggaga gaaatcatag tttaaactgc attataaatt ttataacaga attaaagtag 4500
attttaaaag ataaaatgtg taattttgtt tatattttcc catttggtgact gtaactgact 4560
gccttgctaa aagattatag aagta gcaaa agtattgaa atgtttgcat aaagtgtcta 4620
taataaaact aaactttcat gtg 4643

<210> 259

<211> 486

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(486)

<223> 3' terminal sequence. selectin e
(endothelial adhesion molecule 1) (SELE) gene.

<400> 259

caacctttat agtgttatgt caaataggct tgacataagc tttaaataaat atatacttta 60
aaaattataa aatattttaa gttataattt aaaattctca ataaaactca aacacaaacc 1 20
acactgggat ttcacacagc taattttctaa tgcagtttac ataaatatat acaacttta 180
aacaatttca aagaaaataa cactgtattc catacatagc ctgatcacag tagttgttct 240
ctcttatttc ccagagtttt tctgcccctt taaaagggaac ctctggctgt tctgancctt 300
atcacatctc tgttttgact gttgggcttt ggttgggtgc cagtggttcg gccagggaact 360
tctctgggaa actttttttt tcaacactgg ctagggtang gggngttag gggggnggt 420
ttggtttont cacantocct cagggtnggg ggcgggttng ggggnattacc ggcgggggt 480
tttttc 486

<210> 260
<211> 478
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(478)
<223> 5' terminal sequence. selectin e
(endothelial adhesion molecule 1) (SELE) gene.

<400> 260
gcctactatg ccagatgcct ttatggctga aaccgcaaca cccatcacca cttcaataga 60
tcaaagtcca gcaggcaagg acggccttca actgaaaaga ctcagtgttc cctttcctac 120
tctcaggatc aagaaagtgt tggctaata agggaaggga tattttcttc caagcaaagg 180
tgaagagacc aagactctga aatctcagaa ttcttttctt aactctccct tgctcg ctgt 240
aaaatcttgg cacagaaaca caatatcttg tggctttctt tcttttgccc ttcacagtgt 300
ttcgacagct gattacacag ttctgtcat aaggaatgaa taattaatta tccagagttt 360
agaggaaaaa aatgactaaa aatattatta acttaaaaaa tggacaggtg ttggatgccc 420
acaggcaaat gcatgggggg gttgtttaat gggg gcaaat ccctactga atgctctt 478

<210> 261
<211> 3834
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3834)
<223> selectin e (endothelial adhesion molecule 1)
(SELE) gene.

<400> 261
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ccaaaacgga aagtatttca agcctaaacc ttgggtgaa aagaactctt gaagtcata 120
ttgcttcaca gtttctctca gctctcactt tgggtgcttct cattaagag agtggagcct 180
ggtcttacaa cacctccacg gaa gctatga cttatgatga ggccagtgtt tattgtcagc 240
aaaggtacac acacctggtt gcaattcaaa acaagaaga gattgagtac ctactcca 300
tattgagcta ttcaccaagt tattactgga ttggaatcag aaaagtcaac aatgtgtggg 360
tctgggtagg aaccagaaa cctctgacag aagaagccaa gaactgggct ccaggtgaac 420
ccaacaatag gcaaaaagat gaggactgag tggagatcta catcaagaga gaaaaagatg 480
tgggcatgtg gaatgatgag aggtgcagca agaagaagct tgccctatgc tacacagctg 540
cctgtaccaa tacatcctgc agtggccacg gtgaatgtgt agagaccatc aataattaca 600
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ggtaaaagtt acttattcta gattaccccc tcattgttta ttaacaaatt atgttacatc 2760
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ccacgatgaa aaacttccat gaggccaaac gttttgaact aataaaagca taaatgcaa 3000
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aacaattcca aaggaatctc cagttttcag ttgatcactg gcaatgaaaa attctcagtc 3360
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tttaaatat aacttaaaat attttataat ttttaaagta tataatttat taagcttatg 3780
tcagacctat ttgacataac actataaagg ttgacaataa atgtgcttat gttt 3834

<210> 262

<211> 267

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(267)

<223> 3' terminal sequence. epidermal growth factor (beta-urogastrone) (EGF) gene.

<400> 262

gtttatgttt ttggtgattt tatttaaata attagaagaa attcatcggt gt ctataatg 60

172/292

aaaacaaatc aggcaattta cttacaatct tgtaactgaa aatacatata aattctgtgc 120
aatcacacca agagggaataa ttctgtaggg gaaaaggaca gtaatgacta agaaactccg 180
aagcctcctg tgtaatatct taaaatanaa tgttttcatt caaatatttt aaaaaataag 240
natctaactc gaaaaaatca gtttcta 267

<210> 263

<211> 383

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(383)

<223> 5' terminal sequence. protein kinase c
substrate 80 k-h (PRKCSH) gene.

<400> 263

ggagtccgag gtgcaggggg agcagcccaa gccggccagc cctgctgagn gaagacaaaa 60
tnccgccta cgacgagcag acgcaggcct tcatcgatgc tgcccaggag gcccgcaaca 120
agttcgagga ggccgagcgg tcgctgaagg acatggagga gtccatcagg aacctggnag 180
caaganattt cttttgactt tggccccaac ggnagttttg cttacctgta cagccagtgc 240
tacgagctca ccaccaacga atacgtctac cgcctctncc cttcaagct tgtnttcgna 300
gaaacccaaa ctccgggggt ctcccaccag ccttggcacc tgggggcttc atgggattgg 360
gcccgacca cnacaatttc agt 383

<210> 264

<211> 2056

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2056)

<223> protein kinase c substrate 80k -h (PRKCSH)
gene.

<400> 264

ggaaccgcgg ctgctggaca agaggggtgc ggtggatact gacctttgct ccggcctcgt 60
cgtgaagaca cagcgcattc cccgcgtgta ggcttctccc acagaacccg ttccgggcct 120
cagagcgtct ggtgagatgc tgttgccgct gctgctgctg ctacctatgt gctgggccgt 180
ggaggtcaag aggccccggg gcgtctccct caccaatcat cacttctacg atgag tccaa 240
gcctttcacc tgcctggagc gttcggccac catcccattt gatcaggta acgatgacta 300
ttgcgactgc aaagatggct ctgacgagcc aggcacggct gcctgtccta atggcagctt 360
ccactgcacc aacactggct ataagcccct gtatatcccc tccaaccggg tcaacgatgg 420
tgtttgtgac tgctgcgatg gaacagacga gta caacagc ggcgtcatct gtgagaacac 480
ctgcaaagag aagggccgta aggagagaga gtccctgcag cagatggccg aggtcaccgc 540
cgaagggttc cgtctgaaga agatccttat tgaggactgg aagaaggcac gggaggagaa 600
gcagaaaag ctcattgagc tacaggctgg gaagaagtct ctggaagacc aggtggagat 660
gctgcggaca tgaaggagg aagctgagaa gccagagaga gaggccaaag agcagcacca 720
gaagctgtgg gaagagcagc tggctgctgc caaggcccaa caggagcagg agctggcggc 780
tgatgccttc aaggagctgg atgatgacat ggacgggacg gtctcgggtga ctgagctgca 840
gactcaccgc gagctggaca cagatgggga tggggcggtt tcagaagcgg aag ctcaggc 900
cctcctcagt ggggacacac agacagacgc cacctctttc tacgaccgcg tctgggccgc 960

173/292

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catcaggac aagtaccggt ccgaggcact gccaccgac cttccagcac cttctgcccc 1020
tgacttgacg gagcccaagg aggagcagcc gccagtgcc tcgtcgccca cagaggagga 1080
ggaggaggag gaggaggagg aagaagaggc tgaagaagag gaggaggagg aggattccga 1140
ggaggcccca ccgccactgt caccgccgca gccggccagc cctgctgagg aagacaaaat 1200
gccgccctac gacgagcaga cgcaggcctt catcgatgct gcccaggagg cccgcaacaa 1260
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gagcttgccc tccctgggcc cccaccttg tgactcgcc ccaccaccc cagccct gtc 1980
cctgccaccc ctctagtgg ggactagtga atgacttgac ctgtgacctc aatacaataa 2040
atgtgatccc ccaccc 2056

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<210> 265
 <211> 379
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence :primer

<220>
 <221> misc_feature
 <222> (1)..(379)
 <223> 5' terminal sequence. diphtheria toxin
 receptor (heparin-binding epidermal growth
 factor-like growth factor) (DTR) gene.

```

<400> 265
ggttctgtga cccatctgta gtaatttatt gtctgtctac atttctgc ag atcttccgtg 60
gtcagagtgc cactgcggga ntctgtatgg tcaggatgta ggggttaact tggtcagagc 120
cactctatga gttggacttc agtcttgccct aggcgatttt gtctaccatt tgtgttttga 180
aagcccaagg tgctgatgtc aaagtgtaac agatatcagt gtctccccgt gtcctctccc 240
tgccaagtct cagaagaggc tgggctt cca tgctgttagc ttctctggtc cctcaccccc 300
atggcccccag gccacacgagc tggagactnc actttncctt tgtgtcaaga cattctctcn 360
aactctgnc attcttctg 379

```

<210> 266
 <211> 2360
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(2360)
 <223> diphtheria toxin receptor (heparin-binding
 epidermal growth factor-like growth factor) (DTR)
 gene.

<400> 266

```

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gggcgggctg agtgagcaag acaagacact caagaagagc gagctgcgcc tgggtcccgg 120
ccaggcttgc acgcagaggg gggcggcaga cgggtgcccg cggaatctcc tgagctccgc 180
cgcccagctc tggtgccagc gccagtggtc cgccgcttcg aaagtgactg gtgcctcgcc 240
gcctcctctc ggtgcgggac catgaagctg ctgccgtcgg tgggtgctgaa gctctttctg 300
gctgcagttc tctcggcact ggtgactggc gagagcctgg agcggcttcg gagagggcta 360
gctgctggaa ccagcaaccc ggaccctccc actgtatcca cggaccagct gctaccoccta 420
ggagcgaggc gggacgggaa agtcctgtgac ttgcaagagg cagatctgga cctttt gaga 480
gtcactttat cctccaagcc acaagcactg gccacaccaa acaaggagga gcacgggaaa 540
agaaagaaga aaggcaaggg gctaggggag aagagggacc catgtcttcg gaaatacaag 600
gacttttgca tccatggaga atgcaaatat gtgaaggagc tccgggctcc ctctgcac 660
tgccacccgg gttaccatgg agagaggtgt catg ggctga gcctcccagt ggaaaatcgc 720
ttatatacct atgaccacac aaccatcctg gccgtggtgg ctgtggtgct gtcactctgc 780
tgtctgctgg tcatcgtggg gcttctcatg tttaggtacc ataggagagg aggttatgat 840
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gtatgctgtc atggtcctt ctggaagtt ctgggtgcat ttctgaactg ttacaacttg 2280
tatttccaaa cctggttcat atttatactt tgcaatccaa ataaagataa cccttattcc 2340
ataaaaaaaaa aaaaaaaaaa 2360

```

<210> 267

<211> 435

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(435)

<223> 5' terminal sequence. integrin, beta 2

(antigen cd18 (p95), lymphocyte

function-associated antigen 1; macrophage antigen

1 (mac-1) beta subunit) (ITGB2) gene.

<400> 267

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aggagtgcgc cggtgcgcgc tcacctgtg gcaagtacat ctctgcgcc gagtgctga 60

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```
agttcgaaaa gggccctnt ggaagaactg cagcgcgggc tgtccgggcc tgcagctgtc 120
gaacaacccc gtgaagggca ggacctgcaa ggagaggac tcagag ggct gctgggtggc 180
ctacacgctg gagcagcagg acgggatgga ccgctacctc atctatgtgg atgagagccg 240
agagtgtgtg gcaggcccca acatcgccgc catcgctcggg ggcaccgtgg gcaggcatcg 300
tgctgatcgg cattctcctg ctggtcatct gggaaggctc tgatccacct gagcgacctc 360
cgggagttac aggcgttttg agna ggagaa gctcaagtc cagtnngaac aatgattatt 420
ccctttttca agagc 435
```

<210> 268

<211> 2776

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2776)

<223> integrin, beta 2 (antigen cd18 (p95),
lymphocyte function-associated antigen 1;
macrophage antigen 1 (mac-1) beta subunit) (ITGB2)
gene.

<400> 268

```
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acaccgaggg acatgctggg cctgcgcccc ccactgctcg ccctgggtggg gctgctctcc 120
ctcgggtgcg tctctctca ggagtgcacg aagttcaagg tcagcagctg ccgggaatgc 180
atcagatcgg ggcccggctg cacctgggtgc cagaagctga acttcacagg gccgggggat 240
cctgactcca ttcgctgcga cacccggcc cagc tgctca tgaggggctg tgcgggtgac 300
gacatcatgg accccacaag cctcgctgaa acccaggaag accacaatgg gggccagaag 360
cagctgtccc cacaaaaagt gacgctttac ctgcgaccag gccaggcagc agcgttcaac 420
gtgaccttcc ggcgggccaa gggctacccc atcgacctgt actatctgat ggacctctcc 480
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ctcaacgaga tcaccgagtc cgccgcatt ggcttcgggt ccttcgtgga caagaccgtg 600
ctgcggttcg tgaacacgca ccctgataag ctgcgaaacc catgccccaa caaggagaaa 660
gagtgccagc ccccgtttgc cttcaggcac gtgctgaagc tgaccaacaa ctcc aaccag 720
tttcagaccg aggtcgggaa gcagctgatt tccggaaacc tggatgcacc cgagggtggg 780
ctggacgcca tgatgcaggt cgccgcctgc ccggaggaaa tcggctggcg caacgtcacg 840
cggctgctgg tgtttgccac tgatgacggc ttccatttcg cgggcgacgg aaagctgggc 900
gccatcctga cccccaacga cgccgctgt ca cctggagg acaacttgta caagaggagc 960
aacgaattcg actacccatc gttgggcccag ctggcgca ca agctggctga aaacaacatc 1020
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aggaccactg agggctgcct gaaccgcggc cgtgttgagt gtagtggtcg tggccggtgc 1860
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ggcccctttg ggaagaactg cagcgcgggc tgtec gggcc tcagctgtc gaacaacccc 2040
gtgaagggca ggacctgcaa ggagaggac tcagagggtc gctgggtggc ctacacgctg 2100
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176/292

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gagcagcagg acgggatgga ccgctacctc atctatgtgg atgagagccg agagtgtgtg 2160
gcaggcccca acatcgccgc catcgtoggg ggcaccgtgg caggcatcgt gctgatcggc 2220
attctcctgc tggatcatctg gaaggctctg atccacctga gcgacctccg ggagtacagg 2280
cgctttgaga aggagaagct caagtcccag tggacaatg ataatcccct tttcaagagc 2340
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ctcttgagga tgtcaccaat taaccagaaa tccagttatt ttccgccctc aaaatgacag 2520
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agtctttgca tggagacttg aggagggtt gaggttggtg aggttaggtg cgtgtttcct 2640
gtgcaagtca ggacatcagt ctg attaaag gtggtgccaa tttatttaca tttaaacttg 2700
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aaaataaaac ttcaat 2776

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<210> 269

<211> 449

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(449)

<223> 5' terminal sequence. neogenin (chicken)
homolog 1 (NEO1) gene.

<400> 269

```

ccaggaccct gaaggtgcta ccagctcctc ttacttggcc agctcccaag aggaagattc 60
aggccagagt cttccactg cccatgttcg ccctcccaac ccattgaaga gcttcgccgt 120
gccagcaatc ccgctccag gacctccac ctatgatect gcattgcca gacacaccatt 180
actgtcccag caagctctga accatcacat tcaatcagtg aagacagcct ccacggggac 240
tctaggggaag ggagccggcc tccatgcca gtggtgttc ccagtgcctc t gaagtgcag 300
ggagaccaca aggtgtttg gaaggattnc gagagtaggt attgaaccag ntgaggttga 360
ncaaagagtt gggccatngg gggagggtt aattgaangg gaccttaaac gtttttnac 420
aacagcttga cggacttta acggggggc 449

```

<210> 270

<211> 5297

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5297)

<223> neogenin (chicken) homolog 1 (NEO1) gene.

<400> 270

```

gggcggggcc gggctgggct ggagcagcgg cggccgggag cagagcttgc agcgaggagc 60
cggctgaggc gcgcgggagg gaaggaggca agggctccgc ggcgctgtcg cgctgccgct 120
cactctcggg gaagagatgg cggcggagcg gggagcccgg cgactctca gcaccccctc 180
cttctggctc tactgctcg tgctgctcgg gcgcggggcg cggggcgccg cggcggccag 240
gagcggctcc gcgcgcagct cccaggagc cagcattega acgttcaact cattttattt 300
tctggtggag ccggtggata cactctcagt tagaggctct tctgttatat taaactgttc 360
agcatattct gagcctctc caaaaattga atggaaaaa gatggaactt ttttaactt 420
agtatcagat gatcgacgcc agcttctccc ggatggatct ttatttatca gcaatgttgt 480

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gcattccaaa cacaataa ac ctgatgaagg ttattatcag tgtgtggcca ctgttgagag 540
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 caaagatgtg aaacctccag atctctggat ccatcatgag agactggagc tgaaccat 3660
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 cagagggcat ggtcagag acagcatgtc tacactggct ggaaggcgag gaatgagacc 3840
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 cagtcatctc taccaccogg gcagcccatg gccatttggc acatccatgt ccctttcaga 4020
 cagggccaat tccacagaat ccgttcgaaa tacccccagc actgacacca tgccagcctc 4080
 ttctctcaa acatgctgca ctgatcaca ggaccctgaa ggtgctacca gctcctctta 4140

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cttggccagc tccaagagg aagattcagg ccagagtctt ccca ctgcc atgttcgccc 4200
tccccacca ttgaagagct tcgccgtgcc agcaatccc cctccaggac cccccaccta 4260
tgatcctgca ttgccaagca caccattact gtcccagcaa gctctgaacc atcacattca 4320
ctcagtgaag acagcctcca tcgggactct aggaaggagc cggcctccta tgccagtggg 4380
tggtccccagt gcccctgaa g tgcaggagac cacaaggatg ttggaagact ccgagagtag 4440
ctatgaacca gatgagctga ccaaagagat ggcccacctg gaaggactaa tgaaggacct 4500
aaacgctatc acaacagcat gacgaccttc accaggacct gacttcaaac ctgagtctgg 4560
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tgagaacaca gaatgagcca gcagactggc cagcgctct gtgtagggt ggctccaggc 4680
atggccacct gccttccctt ggtcagcctg gaagaagcct gtgtcaggc agcttccctt 4740
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tcaactgtgag attacagatc tatttgaatt gaatgaaatg taacat tgaa aaaaaaaaaa 5280
aaaaaaaaa aaaaaaa 5297

```

<210> 271

<211> 389

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(389)

<223> 3' terminal sequence. pou domain, class 2,
transcription factor 2 (POU2F2) gene.

<400> 271

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cagggaatn nttcatnatg gaaaaagaca actgaatgcc ctcaactgaa tgtcttcac 60
ccctcttgcc tgaaatttcc accttcccat aggtctggga gggagtcagt tccagagcag 120
aggagggtga cagggttgag gagggacttg tgagagctag aacttgcaa aatggcctag 180
cccaccctc aaaggggaaa agagggagga acaggggatg aaaagttntc cgcagccttc 240
ccttgaactc tcccctgctg ggggagggag gaggttaaag caagacccc tgcccagggtg 300
gggagagctg ggggccaggg gagaagggga caaatggtag ggacacattc tgtttgagca 360
caatgctaaa aattctgtac atcctttgg 389

```

<210> 272

<211> 2048

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2048)

<223> pou domain, class 2, transcription factor 2
(POU2F2) gene.

<400> 272

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```

cgtcaacatg agttgggctt ggggcagatg aggctggctg gcggggcggg cagcatgggt 60
cactccagca tgggggctcc agaaataaga atgtctaagc ccctggaggc cgagaagcaa 120
ggtctggact ccccatcaga gcacacagac accgaaagaa atggacca ga cactaatcat 180
cagaaccccc aaaataagac ctccccattc tccgtgtccc caactggccc cagtacaaag 240
atcaaggctg aagaccccag tggcgattca gcccagcag caccctgcc ccctcagccg 300
gccagcctc atctgcccc ggcceaactc atgttgacgg gcagccagct agctggggac 360
atacagcagc tcctccagct ccagca gctg gtgcttgtgc caggccacca cctccagcca 420
cctgctcagt tcctgctacc gcaggcccag cagagccagc caggcctgct accgacacca 480
aatctattcc agctacctca gcaaaccag ggagctcttc tgacctcca gcccggggcc 540
gggcttccca cacagcccc caaatgcttg gagccaccat cccacccga ggagccagt 600
gatctggagg agctggagca attcgccgc accttcaagc aacgccgat caagctgggc 660
ttcacgcagg gtgatgtggg cctggccatg ggcaagctct acggcaacga cttcagccag 720
acgaccattt cccgcttcga ggcctcaac ctgagcttca agaactgtg caaactcaag 780
ccctcctgg agaagtggct caacgatgca gagactatgt ctgtgg actc aagcctgcc 840
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aagaagagga ccagcatcga gacaaacgtc cgcttcgcct tagagaagag ttttctagcg 960
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gaagtgatcc gcgtctgggt ctg caaccgg cgccagaagg agaaacgcat caaccctgc 1080
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aggaagacc aaaaaaaca ccaacaaaa aaaaaaaa aaaggaaag aaactaacca 1920
acaaaagaga aaacaaaaa taatcacac agaaaccagc tgcccaag gaaccagagg 1980
tgaaaaacaa aaaaaaaaa caaaaaaca accaaaaaa aaaaaaac tctacccct 2040
ctagagcc
2048

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<210> 273

<211> 472

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(472)

<223> 3' terminal sequence. baculoviral iap
repeat-containing 4 (BIRC4) gene.

<400> 273

```

ttttctatct ttccaccagc atggaaca at tgattccttt ttcacacaaa acaaattatg 60
tgattgggga gattaactct aatctccaca ttatatata gaaagctcca tttgttaagc 120
ctatctgaaa agaataaaaa atccagatga ttaattcact tacacttaga aattaaatca 180
gtatactatg aatacacatt gtgttcagtt atagtatgat gcttcttatt cttagtctat 240
ggtttcaatt aaataacagt aaaaaaaatg gataatacag ctaataccct gaaaaatcaa 300
gaaattcaaa gatttatatt ccaactaaaa cactgccatg tacatttttt ttccctacttg 360
gtagcaaatg ctaatggaat tcaatcctga ttacttaaag tcagttcaca tcacacattc 420
aatcagggta ataagaacaa cataacatgc ctaccataga gtttagatta a ga 472

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<210> 274
<211> 2540
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2540)
<223> baculoviral iap repeat -containing 4 (BIRC4)
gene.

<400> 274
gaaaagggtgg acaagtccta ttttcaagag aagatgactt ttaacagttt tgaaggatct 60
aaaacttgtg tacctgcaga catcaataag gaagaagaat ttgtagaaga gtttaataga 120
ttaaaaaactt ttgctaattt tccaagtggt agtctgttt cagcatcaac actggcacga 180
gcagggtttc tttatactgg tgaaggagat accgtgcggt gcttt agttg tcatgcagct 240
gtagatagat ggcaatatgg agactcagca gttggaagac acaggaaagt atcccaaat 300
tgcagattta tcaacggctt ttatcttgaa aatagtgcca cgcagtctac aaattctggt 360
atccagaatg gtcagtacaa agttgaaaac tatctgggaa gcagagatca ttttgcctta 420
gacaggccat ctgagacaca tgc agactat cttttgagaa ctgggcagggt ttagatata 480
tcagacacca tatacccgag gaaccctgcc atgtattgtg aagaagctag attaaagtcc 540
tttcagaact ggccagacta tgctcaocta accccaagag agttagcaag tgctggactc 600
tactacacag gtattggtga ccaagtgcag tgcttttgtt gtggtggaat actgaaaaat 660
tgggaaacct gtgatcgtgc ctggtcagaa cacaggcgac actttcctaa ttgcttcttt 720
gttttgggcc ggaatcttaa tattcgaagt gaatctgatg ctgtgagttc tgataggaat 780
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tatgctttag gtgaagggtga taaagtaaag tgctttcact gtggaggagg gctaactgat 960
tggaagccca gtgaagaccc ttgggaacaa catgctaaat ggtatccagg gtgcaaatat 1020
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gagtgtctgg taagaactac tgagaaaaca ccatcactaa ctagaagaat tgatgatacc 1140
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aagaaaataa tggaggaaaa aattcagata tctgggagca actataaatc acttgagggt 1260
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tattacctg attgaatgtg tgatgtgaac tgactttaag taatcaggat tgaattccat 1620
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attcatagta tactgattta atttctaagt gtaagtgaat taatcatctg gattttttat 1860
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gaaagataga gattgttttt agaggttgggt tgttgtgttt taggattctg tccattttct 2040
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aagtatgtat gttgttaata tgcatagaac gagagatttg gaaagatata caccaaaactg 2280
ttaaatttgg tttctcttcg gggagggggg gattggggga ggggcccag aggggtttta 2340
gaggggcctt ttcactttcg acttttttca ttttgttctg ttoggtttt ttataagtat 2400
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gtgctcttcc tagggagctg tgttgtttcc caccaccac ccttccctct gaacaaatgc 2520
ctgagtgtg gggcactttg 2540

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<210> 275
<211> 842
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(842)
<223> 3' terminal sequence. death associated
protein 3 (DAP3) gene.

<400> 275
tagaaagata ttttattttt taggaaaaga gccataatta tcttaaa tgt gaaaaaccac 60
atccaataaa ctgatataaa gttttaggaa caaggggaata tcttattgtc acgcattcac 120
agtgaaccac attttaatgc aggtccagag ccaactgcag tcctgtccaa tcccataggt 180
acaaggcctt ggctcctctt cctgtgtact gcccgacttc ctcactttac tgggtccagc 240
ataaagcaga tgtccactgt cttcct caca tgctgtgato ttggcttaga ggtaggcaca 300
gtgccgctcc agcagcgagg ggttcgcgtt acttaggaac agcagctctt tttcccttc 360
ttctgtagga gctntctcat gttgaagcca attgttttcc aaataatact gaatacaact 420
ttcaaattcc tttgggttat agttggaaac caggatggga ataaagggat ccagggcac 480
aaatccttcc tttccagca actcctgcgg cagataggct ttccgggct taaagagaga 540
cccagctcgg ctcaagcgc acacaatggc gcctccatgc caatcatnct tcatcatttt 600
cctcagttgt gaacaagtgc taattccctc ggggcaatcg ggctttatct tctgttttca 660
gagggttctt ccccaangag cattgatgcc accacggcca cctatg ggtg aaacataccc 720
caatgaactt tgctcttttag ctctttcagc acaatttcaa actgatctgg tgcgtccctc 780
aaccgtgtta tgccctgtca aaccacttct ccagaagac tccctttctt aggtttttct 840
ct 842

<210> 276
<211> 1608
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1608)
<223> death associated protein 3 (DAP3) gene.

<400> 276
gaattccgcc ggccccaggc agcgtgtgtc ggtcgcttag gctggagaac tagtcct cga 60
ctcacgtgca aggatgatgc tgaaaggaat aacaaggctt atctctagga tccataagtt 120
ggaccctggg cgttttttac acatggggac ccaggctcgc caaagcattg ctgctcacct 180
agataaccag gttccagttg agagtccgag agctatttcc cgcaccaatg agaatgacct 240
ggccaagcat ggggatcagc acgaggggtca gcacta caac atctcccccc aggatttga 300
gactgtatct ccccatggcc ttctctctcg ctttgtgatg caggtgaaga cattcagtga 360
agcttgcttg atggttaagga aaccagccct agaacttctg cattacctga aaaacaccag 420
ttttgcttat ccagctatac gatattctct gtatggagag aagggaacag gaaaaaccct 480
aagtctttgc catgttattc atttctgtgc aaaacaggac tggctgatac tacatattcc 540
agatgtcat ctttgggtga aaaattgtcg ggtcttctg cagtccagct acaacaaaca 600
gcgctttgat caacctttag aggtttcaac ctggctgaag aatttcaaaa ctacaaatga 660
gcgcttcttg aaccagataa aagttcaaga gaagtatgtc tggaataaga gagaaa gcac 720
tgagaaaggg agtctcttgg gagaagtggg tgaacagggc ataacacggg tgaggaacgc 780
cacagatgca gttggaattg tgctgaaaga gctaaagagg caaagttctt tgggtatgtt 840
tcacctcta gtggcgtg atggaatcaa tgctctttgg ggaagaacca ctctgaaaag 900

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agaagataaa agcccgattg ccccgagga atta gcactt gttcacaact tgaggaaaat 960
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ctttaagccc cggaagcct atctgcccc ggagttgctg ggaaaggaag gatttgatgc 1080
cctggatccc tttattocca tcctggtttc caactataac ccaaaggaat ttgaaagttg 1140
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gaaaaaagag ctgctgttcc taagtaacgc gaaccctcgc ctgctggagc ggcactgtgc 1260
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accagtaag atgaggaagt cgggcagtac acaggaagag gagccaggc c cttgtacct 1380
tggtgattgga caggactgca gttggctctg gacctgcatt aaaatgggtt tcactgtgaa 1440
tgctgtacaa taagatatc cttgttcct aaaactttat atcagtttat tggatgtggt 1500
ttttcacatt taagataatt atggctcttt tcctaaaaaa taaaatatct ttctaaaaaa 1560
aaaaaaaaa aaaaaaaaaa aaa aaaaaa aaaaaaaaaa aaaaaaa 1608

<210> 277

<211> 361

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(361)

<223> 5' terminal sequence. gonadotropin -releasing hormone 1 (leutinizing -releasing hormone) (GNRH1) gene.

<400> 277

ttagattgca tgctattgta tgtctacagg gcatttgaca gccaaggnat aaatccagg 60
gggacgggat ctaatgatgt cctgtccttc actgtccttg ccacaccag ccacagagat 120
ccaggctttg gggactccca cagcttatcg accag tgttt gatttagttt ttagcctctt 180
tcccatcaaa tgaaaattaa cttggagaca catttcatta gaaaattaga ggcccccttg 240
gctaggaagg catctggtct gggactaac tactttgaac agtgttgagt cctctctccc 300
acagatgggt cagccagcag taatgctnag ggaagactga agggatcaaa taganaaatg 360
t 361

<210> 278

<211> 470

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(470)

<223> gonadotropin-releasing hormone 1 (leutinizing -releasing hormone) (GNRH1) gene.

<400> 278

gggatctttt tggtctctctg cctctaaca gaatgaagcc aattcaaaaa ctcttagctg 60
gcctattct actgacttgg tgcgtggaag gctgtccag ccagcactgg tcctatggac 120
tgcgccctgg aggaagaga gatgccgaaa atttgattga ttctttcca a gagatagtca 180
aagaggttgg tcaactggca gaaacccaac gtttcgaatg caccacgcac cagccacgtt 240
ctccccctcg agacctgaaa ggagctctgg aaagtctgat tgaagaggaa actgggcaga 300
agaagattta aatccattgg gccagaagga atgaccatta ctaacatgac ttaagtataa 360
ttctgacatt gaaaatttat aacccat taa atacctgtaa atggtatgaa tttcagaaat 420

ccttacacca agttgcacat attccataat aaagtgtgt gttgtgaatg

470

<210> 279

<211> 320

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(320)

<223> 3' terminal sequence. interleukin 2
receptor, gamma (severe combined immunodeficiency)
(IL2RG) gene.

<400> 279

ntctaaatat caacagaaac tttatttctc atcggttcag gaacaatcgg agggtagatg 60
gaaagaggaa gggagggaaa gagggaggga ggaagaatcc tgcgaaaagg aagggccaga 120
ctgagggaga agaaaaacat gttcggggca aaagggtaat tctcaagtgg ggaatgccaa 180
atgaaggggt gcttacatgg gggcacaaaa ttccaaatca gccacagtgg ggtgaggtga 240
gtatgagacg caggtggggt tgaatgaagg aaagttagta ccncttaggg ctacaggacc 300
ctggggttct tctttcag ag 320

<210> 280

<211> 407

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(407)

<223> 5' terminal sequence. interleukin 2
receptor, gamma (severe combined immunodeficiency)
(IL2RG) gene.

<400> 280

attcggcaca gggaaactttt cggcctggag tgggtgtgtct aagggaactgg ctgagagtct 60
gcagccagac tacagtgaac gactctgcct cgtcagttag attcccccaa aaggaggggc 120
ccttggggag gggcctgggc tncctcatgc aaccagcata gccctactg ggcccccca 180
tgttacacc taaagcctga aacctgaacc ccantactct gacagaagaa ccccagggtc 240
ctgtagccct aagtggtagt aactttcctt cattcaacc acctgcgtct tatactcanc 300
tcanccact gttggctgat tttggatttt tgtggcccca tgtaaggaac cctttaattt 360
ggcattnccc aattgagaat taaccttttt gncccgaaca tgttttt 407

<210> 281

<211> 1451

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature
<222> (1)..(1451)
<223> interleukin 2 receptor, gamma (severe combined immunodeficiency) (IL2RG) gene.

<400> 281
gaagagcaag cgccatgttg aagccatcat taccattcac atccctctta ttcctgcagc 60
tgccctgtgt gggagtgggg ctgaacacga caattctgac gcccaatggg aatgaagaca 120
ccacagctga tttcttctctg accactatgc ccactgactc cc tcagtgtt tccactctgc 180
ccctcccaga ggttcagtgt tttgtgttca atgtcgagta catgaattgc acttggaaca 240
gcagctctga gccccagcct accaacctca ctctgcatta ttggtacaag aactcggata 300
atgataaagt ccagaagtgc agccactatc tattctctga agaaatcact tctggctgtc 360
agttgcaaaa aaaggagatc cacctctacc aaacatttgt tgttcagctc caggaccac 420
gggaacccag gagacagggc acacagatgc taaaactgca gaatctgggtg atcccctggg 480
ctccagagaa cctaacactt cacaactga gtgaatccca gctagaactg aactggaaca 540
acagattctt gaaccactgt ttggagcact tgggtgcagta ccggactgac tgggaccaca 60 0
gctggactga acaatcagtg gattatagac ataagttctc cttgcctagt gtggatgggc 660
agaaacgcta cacgtttcgt gttcggagcc gctttaacct actctgtgga agtgctcagc 720
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cttctccctc agtctggccc ttcttttctg caggattctt cctccctccc tctttcctc 1380
ccttctctt tccactacc ctccgattgt tctgaaccg atgagaaata aagtttctgt 1440
tgataatcat c 1451

<210> 282
<211> 317
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(317)
<223> 3' terminal sequence. death associated protein 3 (DAP3) gene.

<400> 282
atctaacaca acactttaga aagatatttt attttttagg aaaagagcca taattatctt 60
aaatgtgaaa aaccacatcc aataaactga tataaagttt taggnacaag ggaatatctt 120
attgtcacgc attcacagt aaaccattt taatgcaggt ccagagccaa ctgcagtcct 180
gtccaatccc ataggttaca agggcctggg ctctcttccc tgtgtactgc ccgacttcc 240
catcttactg gggccagca taaagcagga tgcactgt ctctctcaca tgctgtganc 300
ttggncttag gagtag 317

<210> 283
<211> 358
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(358)
<223> 5' terminal sequence. death associated
protein 3 (DAP3) gene.

<400> 283
aggacgggcg ctttgagacc ggccccaggc agcgtgtgtc ggtcgcctag tctggagaac 60
tagtcctcga ctcacgtgca aggatgatgc tgaaaggaat aacaaggctt atctctagga 120
tccataagtt ggacctctgg cgttttttac acatggggac ccaggctcgn caaagcattg 180
ctgctcacct agataaccca ggttcccagt tgagagtccc gagagctatt ttcccgcaac 240
caatgagaat gaccccgggc caagcatggg ggatcancaa ggagggtcaa gcaa tnacaa 300
canttttccc cccaggattt tgggagaatt gtaattttcc ccatnggcct ttncttcc 358

<210> 284
<211> 416
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(416)
<223> 5' terminal sequence. ptk2 protein tyrosine
kinase 2 (PTK2) gene.

<400> 284
gcacagaagc tattgaactc tgacctgggt gagctcatca acaagatgaa actggcccag 60
cagtatgtca tgaccagcct ccagcaagag tacaaaaagc aaatgctgac tgctgctcac 120
gccctggctg tggatgccaa aaacttactc gatgtcattg a ccaagcaag actgaaaatg 180
cttgggcaga cgagaccaca ctgagcctcc cctaggagca cgtcttgcta cctctttttg 240
aagatgttct ctagccttcc accagcagcg agganttaac cctgtgtcct cagtncgcca 300
gcacttacag ctccaacttt tttgaatgac catctgggtt aaaaatcttt ctcatataag 360
tttnaaccac atttggattt ggggttcatt tttgttttg ttttttttc aatcat 416

<210> 285
<211> 3052
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3052)
<223> ptk2 protein tyrosine kinase 2 (PTK2) gene.

<400> 285
ccggtgtgaa ggccatgagt gattactggg ttgttggaag gaagtctaac tatgaagtat 60
tagaaaaaga tgttggttta aagcgatttt ttccctaagag ttactggat tctgtcaagg 120
ccaaaacact aagaaaactg atccaacaaa catttagaca atttgccaac cttaatagag 180
aagaaagtat tctgaaattc tttgagat cc tgtctccagt ctacagattt gataaggaat 240
gcttcaagtg tgctcttggg tcaagctgga ttatttcagt ggaactggca atcgcccag 300

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aagaaggaat cagttaccta acggacaagg gctgcaatcc cacacatctt gctgacttca 360
ctcaagtgca aaccattcag tattcaaaaca gtgaagacaa ggacagaaaa ggaatgctac 420
aactaaaaat agcagggtgca cccgagcctc tgacagtgcac ggcaccatcc ctaaccattg 480
cggagaatat ggctgaccta atagatgggt actgccggct ggtgaatgga acctcgagcgt 540
catttatcat cagacctcag aaagaagggt aacgggcttt gccatcaata ccaaagttgg 600
ccaacagcga aaagcaaggc atcgggacac acgccgtctc tgtgtcag aa acagatgatt 660
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ctagccttcc accagcagcg aggaattaac cctgtgtcct cagtcgccag cactcacagc 2760
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gatccaaaat gtggcgtttt tctaagaatg aaaattatat gtaagctttt aagcatcatg 2940
aagaacaatt tatgttcaca ttaagatacg ttctaaagg ggaatggcaa ggggtgacat 3000
cttaattcct aaactacctt agctgcatag t ggaagagga gagccggaat tc 3052

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<210> 286

<211> 377

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(377)

<223> 3' terminal sequence. cyclin -dependent
kinase 4 (CDK4) gene.

<400> 286

gnataaaaaa ggaccccaaa tataaaggna gggaaaggga caagaggga catacccctt 60
agtgtagaga aatgggaagg agaaggagaa gcctcaaaag gaggtgggag gggaatgtca 120
ttaaggcagc aaagtaatct ctgtagaaag atggaggagg accctccata gcctcagaga 180
taaaggcaaa gattgccctc tc agtgtcca gaagggaat gggcagcttt tcttcntcc 240
atgggcagcg actccattgc tctcccggn ttaccttcat ccttatgtag gataagagtn 300
ctgcagagct tcgaaagggc agagattcgc ttgtgtggg ttaaaagtca gcatttccan 360
cagcagcttt tgcttcc 377

<210> 287

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(363)

<223> 5' terminal sequence. cyclin -dependent
kinase 4 (CDK4) gene.

<400> 287

catatctgga caaggcacc ccaccaggct tgcagccgaa acgatcaagg atctgatgcg 60
ccagtttcta agaggcctag atttccttca tgccaattgc atcggtcacc gagatctgaa 120
gccagagaac attctggtga caagtggtna aacagtcaag ctggctgact ttngcctggc 180
cagaatctac agctaccaga tggcacttac acccggtggtt gttacactct ggtacc gagc 240
tcccgaagtt cttctngcag tccacatatg caacacctgt gggacatgtg ggagtgttg 300
ctgtatcttt gcagagatgt ttcgtcgaaa ncctctcttt ctgtggnaaa ctctgtaagg 360
ccg 363

<210> 288

<211> 1443

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1443)

<223> cyclin-dependent kinase 4 (CDK4) gene.

<400> 288

gccctcccag tttccgcgcg cctctttggc agctgggtcac atgggtgagg tgggggtgag 60
ggggcctctc tagcttgcgg cctgtgtcta tggctgggcc ctctgcgtcc agctgctccg 120
gaccgagctc ggggtgtatg gccgtagga accggctccg gggcccgat aacgggcgc 180
ccccacagca ccccgggctg gcgtgagggt ctcccttgat ctgagaatgg ctacctctcg 240
atatgagcca gtggctgaaa ttggtgtcgg tgcctatggg acagtgt aca aggcccgta 300
tcccacagt ggcactttg tgccctcaa gagtgtgaga gtcccaatg gaggaggagg 360
tggaggaggc cttcccatca gcacagttcg tgagggtggt ttactgaggc gactggaggc 420
ttttgagcat cccaatgttg tccggctgat ggacgtctgt gccacatccc gaactgaccg 480
ggagatcaag gtaaccctgg tggtt gagca tgtagaccag gacctaagga catatctgga 540
caaggcacc ccaccaggct tgccagccga aacgatcaag gatctgatgc gccagtttct 600
aagggccta gatttccttc atgccaattg catcggtcac cgagatctga agccagagaa 660
cattctggtg acaagtggtg gaacagtcaa gctggctgac tttggcctgg ccagaatcta 720

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cagctaccag atggcactta caccogtggg ttgtacactc tggtagcgag ctcccgaagt 780
tcttctgcag tccacatatg caacacctgt ggacatgtgg agtggtggct gtatctttgc 840
agagatgttt cgtcgaaagc ctctcttttg tggaaactct gaagccgacc agttgggcaa 900
aatctttgac ctgattgggc tgcctccaga ggatgactgg cctcg agatg tatccctgcc 960
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tgcctttcga gctctgcagc actcttatct acataaggat gaaggtaatc cggagtgage 1140
aatggagtggt ctgccatgga aggaagaaaa gctgccattt cccttctgga cactgagagg 1200
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ttccatttc tctacactaa ggggtatgtt ccctctgtc cctttcccta cctttatatt 1380
tggggctcctt ttttatagc gaaaaacaaa accaaaagaa awaatggccc tttttttttt 1440
ttt 1443

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<210> 289

<211> 394

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(394)

<223> 3' terminal sequence. basic transcription
factor 3 (BTF3) gene.

<400> 289

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ccgcgctgtg tgcgcctaan ctcagngnngn ccacccgaga ccccttgagc accaacccta 60
gtccccgcgc cggcccctna ttgcctccga caagatgaaa gaaaca atca tgaaccaggg 120
aaaactcgcc aaactgcagg cacaagtgcg cattggtggg aaaggaactg ctgcgagaaa 180
gaagaagggtg gttcatagaa cagccacagc agatgacaaa aaacttcagt tctccttaaa 240
gangttaggg gtaacaata tctctggnat tgaagagggtg aatatgttta caaaccaggg 300
aacagtgatc cactttaaca acc tnaagt tcagggcatc tctgggcagc ggacactttc 360
accattacng gccttgctga gncaaagcag ctgg 394

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<210> 290

<211> 477

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(477)

<223> basic transcription factor 3 (BTF3) gene.

<400> 290

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atgcgacgga caggcgcacc cgctcaggct gactctcggg ggcgagggtc agccaggggc 60
ggctgccctg ggggcgaggc gacgtgtct caacctccac ctgcggcgg aaccgagga 120
gaggagcctc agatgaaaga aacaatcatg aaccag gaaa aactcgccaa actgcaggca 180
caagtgcgca ttggtgggaa agtgaatatg tttaaaaacc aaggaacagt gatccacttt 240
aacaacccta aagttcaggc atctctggca gcgaacactt tcaccattac aggccatgct 300
gagacaaaag agctgacaga aatgctaccc agcatcttaa accagcttgg tgcggatagt 360
ctgactagtt taaggagact ggccgaagct ctgcccaaac aatctgtgga tggaaaagca 420
ccatttgcta ctggagagga tgatgatgat gaagttccag gaggttcca agaata 477

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<210> 291
<211> 388
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(388)
<223> 3' terminal sequence. colony stimulating
factor 1 receptor, formerly mcdonough feline
sarcoma viral (v-fms) oncogene homolog (CSF1R)
gene.

<400> 291
tgctgttagt ttaatgtgga cagagacatc ccacggcgtg actgttagt t aggatgagtc 60
agcttggggg agtttgtgct tcctgcttgg ngtggccagc cacatgccaa ggtcccctgc 120
cttctagccc agaatgacgg gactgggagc aacaccccca acttttagct gccacttggc 180
tcattacagc agtaccagta tgggggtggg aggggtgagg cnttggagtg aaggcggcgt 240
atagggcaga gactaagagg gtcctgtg ag attcttagag gagccatcct gntccaagg 300
gcctgagctg agtntgggtc tgtgagcatc tgctgctcct ctcagagagg ggagatctca 360
ctctctgcca gtctgtctag ccccaaag 388

<210> 292
<211> 3992
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3992)
<223> colony stimulating factor 1 receptor,
formerly mcdonough feline sarcoma viral (v-fms)
oncogene homolog (CSF1R) gene.

<400> 292
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ggagaagaga gaagaggaag aggaagagga agagaggaag cggagggaac tgcggccagg 120
ctaaaagggg aagaagagga tcagcccaag gaggaggaag aggaaaacaa gacaaacagc 180
cagtgcagag gagaggaacg tgtgtccagt gtcccgatcc ctgcggagct agtagctgag 24 0
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tctttggggc tagacagact ggcagagagt gagatctccc tctctgagag gagcagcaga 3660
tgctcacaga ccacactcag ctacggccc ttggagcagg atggtcctc taag aatctc 3720
acaggacctc ttagtctctg ccctatacgc cgccttact ccacagcctc acccctccca 3780
ccccatact ggtactgctg taatgagcca agtggcagct aaaagtggg ggtgttctgc 3840
ccagtcccgt cattctgggc tagaaggcag gggaccttg cattggctgg ccacaccaag 3900
caggaagcac aaactcccc aagctgact c atcctaacta acagtcacgc cgtgggatgt 3960
ctctgtccac attaaactaa cagcattaat gc
3992

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<210> 293

<211> 356

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

191/292

<221> misc_feature
<222> (1)..(356)
<223> 3' terminal sequence. friend leukemia virus
integration 1 (FLI1) gene.

<400> 293
tttatttagt caaattatatt tacaacatgg ncttctttga cagttgtcag cttaacactt 60
aatatagtta aaaaagtcaa caattacctg caaaattata tataatntnaa tgtctaaaaa 120
tatgtngctt atatagagca ggaaaatccc tcctctccac aagggaagt ttcggtgttt 180
tncccagagc tgtgattatn gcagtactgt tacacgcatt tccaaagcat taaagancta 240
aatgggatta tctttncct gcttgtgtat gcctgtnaaa taactgtacc agtggctttg 300
ctttctcata ggtcagtgc ttaaacagcc ctgtttcctt ttcggctata g ggcatt 356

<210> 294
<211> 465
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(465)
<223> 5' terminal sequence. friend leukemia virus
integration 1 (FLI1) gene.

<400> 294
gaccaaagca gtttcttgtc aatacacggg gttcagtatg acacagaatc atggacttaa 60
cccgtcatgt tctggtttga gatttagtga caaatagagg tgggaagctt ataactaat 120
tttaggagga ccaaattcag tggatggcaa ctggaacatt gattgtaagg ccagtgaagt 180
tttcacccaa ctggaatttg atggaagaa ggtt tgtgtg tttaagacgc caagggcatt 240
gcagaatccc tctcagtgga cagtatgcac tcagctgacc actctctcta gccaatagtc 300
aagatatgga actaaggaaa ttttaatgcc aaattacata cattcctgaa agacggggga 360
attaaattna ctaattttnt tttttttttt ttaaattgatn gacagtggnt ccccggaact 420
tgggaaangt tgtaggggnt ttctaaaccc aagncgattc gcant 465

<210> 295
<211> 2957
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2957)
<223> friend leukemia virus integrati on 1 (FLI1)
gene.

<400> 295
gaattcccaa acgtgcacag gggagtgagg gcagggcgct cgcagggggc acgcaggag 60
ggcccagggc gccagggagg ccgcgccggg ctaatccgaa ggggctgcga ggtcaggctg 120
taaccgggtc aatgtgtgga atattggggg gctcggctgc agacttggcc aaatggacgg 180
gactattaag gaggctctgt cggtggtgag cgacgaccag tccctctttg actcagcgta 240
cggagcggca gccatctcc ccaaggcga catgactgcc tcggggagtc ctgactacgg 300
gcagccccac aagatcaacc ccctcccacc acagcaggag tggatcaatc agccagtgc 360
ggtcaacgtc aagcgggagt atgaccacat gaatggatcc agggagtctc c ggtggactg 420

192/292

```

cagcggttagc aaatgcagca agctggtggg cggaggcgag tccaacccca tgaactacaa 480
cagctatatg gacgagaaga atggccccc tcctcccaac atgaccacca acgagaggag 540
agtcacgtgc cccgcagacc ccacactgtg gacacaggag catgtgaggc aatggctgga 600
gtgggccata aaggagtaca gcttgatgga gatcgacaca tcctttttcc agaacatgga 660
tggcaaggaa ctgtgtaaaa tgaacaagga ggacttcctc cgcgccacca ccctctacaa 720
cacggaagtg ctgttgtcac acctcagtta cctcagggaa agttcactgc tggcctataa 780
tacaacctcc cacaccgacc aatcctcacg attgagtgtc aaagaagacc cttcttatga 840
ctcagtcaga agaggagctt ggggcaataa catgaattct ggctcaaca aaagtccctc 900
ccttgagggg gcacaaacga tcagtaagaa tacagagcaa cggccccagc cagatccgta 960
tcagatcctg ggcccgaaca gcagtcgct agccaaccct ggaagcgggc agatccagct 1020
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ggggaccaac ggggagttca aaatgacgga ccccgatgag gtggccaggc gctggggcga 1140
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cgtgccttca cacttaggca gctactacta gaagcttctt ctactgaag cccatcctgc 1560
acacttactg gatgctttgg actcaacagg acatatgtgg ccttgaaggg aagacaaaac 1620
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agcagtttct tgtcaataca cggggttcag tatgacacag aatcatggac ttaaccctgc 1920
atgttctggt ttgagattta gtgacaaata gagtgaggaa gcttataatc taattttagg 1980
aggaccaaat tcagcgatg gcaactggaa cattgattgt aaggccagtg aagttttcac 2040
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tcctctcag tggacagtat gcactcagct gaccactctc tctagaaata gtcaagatat 2160
gaactaagaa attttaatgc aaatacatat attcctgaaa gacggggaat taaattacta 2220
attttttttt tttaaatgat gacagtgtgc ccagaacttg gaaaagttgt agggatttct 2280
aaactcaagc agattcgcaa gtgctgtgcg cttgtcagac catcagacca gggccaacca 2340
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aaaaataaaa taattaaaaa ttaagaataa ataaacgagt tgacctcgtt cacaaaagca 2460
gttttactat cgaatcaatc gctgttattt ttttttaatg taatttgtac atcttttttc 2520
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cctatagctg aaaaaggaaac agggctgttt aagtcaactg cttatgagaa agcaaagcac 2640
tggtacagtt atttaacagg catacacaag cagggaaaag ataatccatt tagatcttta 2700
atgctttgga aatgcgtgta acagtactgc aataatcaca gctctgggaa aaacaacgaa 2760
actttccctt gtggagagga gggattttcc tgctctata t aagcaacata ttttagaca 2820
ttaaaatata tataattttg caggtaattg ttgacttttt taactatatt aagtgttaag 2880
ctgacaactg tcaaagaaga ccatgttgta aaataatttg actaaataaa tggttccttc 2940
tctcaaaaaa aaaaaaa 2957

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<210> 296

<211> 400

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(400)

<223> 3' terminal sequence. ests, highly similar
to tvhume hepatocyte growth factor receptor
precursor [h.sapiens] (EST R97218) gene.

<400> 296

193/292

```
caccccttct cttcacagat cacgaagatc ccattgaatg gcttgggctg cagacatttc 60
cagtcctgca gtcaatgcct ctctgcccc aaccttgttc agtggtgctg gtgcaganca 120
aatgtgtgcg atcggaggaa tgcctgagcg ggacatggac tcaacagatc tgtctgcctg 180
caatctacaa ggtagggaatc tctaacagct ggcatacatg tttttgtttg gtgttttttt 240
tttttttttg gtttggtttg gtttggtttt tgttttttta gatacaaac ccactaatga 300
aaaaaattta aaaatcaatt tactcattta ggctgtgagg tcatcaggct aaagcaccat 360
ctctctcttg ggctttatcc ctggggcagg ggagggggg 400
```

<210> 297

<211> 464

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(464)

<223> 5' terminal sequence. ests, highly similar
to tvhume hepatocyte growth factor receptor
precursor [h.sapiens] (EST R97218) gene.

<400> 297

```
cggtgtagat ttcatagtg ccgaatatat gcttaagcaa ataaggcaac acagtttagca 60
tggtgcatg gttagccaat gtccattgcc agaaactgag ttctctatca gcaagagatg 120
tgctcatctt gttctggact atatctctc a gggactaga gggcagcctg ctaaattgta 180
tgcaactcaat aaatattttt ggaatgaatt aaagagtggc atggcttaca gaagtataga 240
tgtaggtata gtcacccgtt gagcctttgc ttttttttct gggaacactg aaggaagact 300
cacagccacc catgggtgtt tgaccctcca ctgacctgc ccacctcacc ccgggaaata 360
atcttcagtc tcatctgtgg aacagacaag gccacntct atggcttcgg nacaggtagn 420
aaaactgtcc tgtgtggccc cgctnggcag ggatcaccag ttgt 464
```

<210> 298

<211> 378

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(378)

<223> 3' terminal sequence. ets variant gene 5
(ets-related molecule) (ETV5) gene.

<400> 298

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aaataccaaa actacaaaaa tcagtttata aactgttttt ccaaaacaac caccaaaaaca 60
aaacaatccc ccaaatcagg gcaaaacaaa atactgtcaa aagtgttaat cgcccttctc 120
ctaaaataaa agtcatccac actcagccac gtgattggga agagaaaggg ggcttgctct 180
acttgccgac cacatggccg ggtggttccc aagagtagcc atggtttatg attttgagaa 240
ccacggaggg gnaaacagc tgttctgact gcccccttt ttctagacaa ggggtaatat 300
ttcagattca gctagaagag ctttocaat g tttaagatgt atttttaanc cttaatggtt 360
tnaggcctcc ccaacttt 378
```

<210> 299

<211> 317

194/292

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(317)

<223> 5' terminal sequence. ets variant gene 5
(ets-related molecule) (ETV5) gene.

<400> 299

```
actggaagag gttgctcggc gctggggcat ccagaagaac cggccagcca tgaactatga 60
caagctgagc cgctctctcc gctattacta tgaaaagggc atcatgcaga aggtggctgg 120
agagcgatac gtctacaaat ttgtctgtga cccagatgcc ctcttctcca tggctttccc 180
ggataaccag cgtccgttcc tgaaggcaga gtccgagtgc cacctcagcg aggaggacac 240
cctgccgctg acccactttg aagacagccc cgcttacctc ctggacatgg accgctgcag 300
cagcctcccc tatgccg                                     317
```

<210> 300

<211> 4071

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4071)

<223> ets variant gene 5 (ets -related molecule)
(ETV5) gene.

<400> 300

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gagtccagcc gctggtgcgc ggagcgggtc accgtcttcg gagcgggttc gccagcctt 60
tcgccagggc gccagggccc gctgcgcgcg tgcgtgagcg cgcctgcgcc gccagggccg 120
ctgcaagggg aggagagcgg cgcctcagg aggatccctt ttccccaga aattactcaa 180
tgctgaaacc tctcaaagtg gtattagaga cgctgaaagc accatggacg ggttttatga 240
tcagcaagtc ctttttatgg tcccagggaa atctcgatct gaggaatgca gagggcggcc 300
tgtgattgac agaaagagga agtttttga cacagatctg gctcacgatt ctgaagagct 360
atttcaggat ctacgtcaac ttcaagaggc ttggttagct gaagcacaag ttcctgatga 420
tgaacagttt gtcccaga tt ttcagtctga taacctggtg cttcatgccc cacctccaac 480
caagatcaaa cgggagctgc acagcccctc ctctgagctg tcgtcttgta gccatgagca 540
ggctcttggt gctaactatg gagaaaagtg cctctacaac tattgtgcct atgataggaa 600
gcctccctct gggttcaagc cattaacccc tcctacaacc cccctctcac ccacccatca 660
gaatccccta tttccccac ctcaggcaac tctgccacc tcagggcagc cccctgcagc 720
tggtccagtt caaggtgtgg gccccgcccc cgcccccat tcgcttcagc agcctggacc 780
acagcagcaa acatttgcg tcccccgacc accacatcag cccctgcaga tgccaaagat 840
gatgcctgaa aaccagtatc catcagaaca gagatttc ag agacaactgt ctgaacctg 900
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cattgcctgg acaggtcgag gcatggagt caagctgata gaaccggaag aggttgctcg 1440
gcgtgggggc atccagaaga accggccagc catgaactat gacaagctga gccgctctct 1500
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195/292

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ccgctattac tatgaaaagg gcatcatg ca gaaggtggct ggagagcgat acgtctacaa 1560
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cctgaaggca gagtccgagt gccacctcag cgaggaggac accctgccgc tgaccactt 1680
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ctttgagtat tatctggaga acccaagctg tctctggatt ggcaccctta aagacagata 1920
cattggctgg ggagtgggaa cagggagggg cagaaaacca c aaaaaggcc agtgcctcaa 1980
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aattattctc attgctgtat tatattggaa aagtttttaa caaccaagct aaagctatgt 3180
gaaagttgag ctcaaagtag aggaaaagtt actggtggta ccttgcctgc tgctctgctg 3240
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gaacctgccg gctgatttga aatactttca cctgcgcag ggcggtatgc atcctgccaa 4020
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```

<210> 301

<211> 407

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(407)

<223> 3' terminal sequence. cyclin -dependent
kinase 4 (CDK4) gene.

<400> 301

```

nccngtataa aaaaggaccc caaatataaa gtaggggaaa gggacaagag ggaacata cc 60

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196/292

ccttagtgta gagaaatggg aaggagaagg agaagcctca aaaggngagg tgggagggga 120
atgtcattaa ggcagcaaag taatctctgt agaaagatgg aggaggacc tccatagcct 180
cagagnataa ggcaaagntt gccctctcag tntccngaag ggaaatggca gcttttcttc 240
cttccatggg cagccactcc attgctcact ccggatt acc ttcaccccta tgtaggataa 300
gggtgctgca gagctcgaaa gggcagagat tcgcttntgt ggggttaaaa gtcagccttt 360
nccgcagca gctttgcttc cccgactcct nccttttcag gnacccc 407

<210> 302

<211> 405

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(405)

<223> 5' terminal sequence. cyclin -dependent
kinase 4 (CDK4) gene.

<400> 302

attcgncaca gaggaggagg tggaggaggc cttcccatca gcacagttcg tgaggtggct 60
ttactgaggc gactggaggc ttttgagca t cccaatgttg tccggctgat ggacgtctgt 120
gccacatccc gaactgaccg ggagatcaag gtaaccctgg tgtttgagca tgtagaccag 180
gacctaaagga catatctgga caaggcacc ccaccaggct tgccagccga aacgatcaag 240
gatctgatgc gccagtttct aagaggccta gatttccttc atgccaattg catcgttcac 300
cgaggatctg aagccagaga acattctggg tgacaagtgg ttggancagt caagctggct 360
ggactttggg cctgggcagn aatctancag cttaccagat gggca 405

<210> 303

<211> 420

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(420)

<223> 3' terminal sequence. v -yes-1 yamaguchi
sarcoma viral oncogene homolog 1 (YES1) gene.

<400> 303

caatgagaac tttttatttc aattatccac aaaacaatat tacaatactt tataaaaaata 60
ttaagttag gctaccatta ttcatttaaa aaagtgtgct agaaggctgt ttttgccaac 120
ttcctttttt ggtaagggtt aacttccaca ttaagacact gaagacgaaa agctgttggt 180
aaaatatctc caaatttaca aagttgtttt tcttgggcaa tttaaaaata caggancaat 240
ttaaantgaa tacacattaa ggttaggtgt tttatcccta ctatacaatt gttattatat 300
agggaaactgc tcccttcn gg ttaaanccct aatggaatac ccatcaactt ttcccggccc 360
ntactttccc nggattgggg tttagggtac ctaaacggga aatttaggtc nccccnttg 420

<210> 304

<211> 4517

<212> DNA/RNA

<213> Artificial Sequence

197/292

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4517)

<223> v-yes-1 yamaguchi sarcoma viral oncogene
homolog 1 (YES1) gene.

<400> 304

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gtaggcgccg gaagcgctgg ggcgccggag ccgggcccgc gtggcccagag ttccggtgag 180
cggacggcgg cgcgcgcgaga tttgataatg ggctgcatta aaagtaaaga aaacaaaagt 240
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tatggagcag aaccactac agtgtcacca tgtccgtcat ctt cagcaaa gggaacagca 360
gttaatttca gcagtctttc catgacacca tttggaggat cctcaggggt aacgcctttt 420
ggaggtgcat ctctctcatt ttcagtgttg ccaagttcat atcctgcttg tttaacaggt 480
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198/292

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gttatggcctt cacattcatt gcagtgggat atgggttttta tgtaaaacat ttttagaact 3120
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ctgctcccca gggtcacacc attctcctgc ctgagcctcc cgagtagctg ggactacagg 3300
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<210> 305

<211> 459

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(459)

<223> 3' terminal sequence. interferon -induced protein 75, 52kd (IFI75) gene.

<400> 305

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ncttgtctga aggtgtgctg gacacctcct ggggctcttc tgggtcattt gggtctggag 60
aattatctct tatctctggc atagagcccc agggagagtg gggcatctct tgagggtctt 120
ctttatctct tatttggggg atcagggttg cactggccac ttgcacagtg ctagtgagga 180
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gggctgggag actcactcag gatctcatcg ctttgctggg agg atgttcc agggctcact 360
gactcttggg cgcacaaggt gaaacagctt ggtttgaagg gggttnttgg tngggggcaa 420
gcncaatngg gtatggaagg aagcttccct ctaanaagg 459

```

<210> 306

<211> 370

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

199/292

<221> misc_feature
<222> (1)..(370)
<223> 5' terminal sequence. interferon -induced
protein 75, 52kd (IFI75) gene.

<400> 306
tgcgtttgtc aaagcacaga cttcctgttt tgcctgctag catctccctg taactctccc 60
aatcttgagg agtgatccct gtccc agccc ctggaaaggg anggaaacga caaactcaaa 120
gtccaggatg ttcacccatga caagagccat ggaagaggct ctttttcagc acttcatgca 180
ccagaagctg gggatcgctt atgccatata caagccattt cccttctttg aaggcctcct 240
agacaactcc atcatcacta agagaatgta catggaatct ctggaagcct gtagaaattt 300
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ctgtntcttt 370

<210> 307
<211> 1541
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1541)
<223> interferon-induced protein 75, 52kd (IFI75)
gene.

<400> 307
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tccaggaagg aagaagcact tcagtgaacca atgacaagtt aacatccaaa atgaatgcgg 180
aagaagactc agaagagatg cccagcctcc tccactagcac tgtgcaagtg gccagtgaca 240
acctgatccc ccaaataaga gataaagaag accctcaaga gatgccccac tctcccttgg 300
gctctatgcc agagataaga gataattctc cagaacccaa t gacccagaa gagccccagg 360
aggtgtccag cacaccttca gacaagaaag gaaagaaaag aaaaagatgt atctggtcaa 420
ctccaaaaag gagacataag aaaaaaagcc tccaagagg gacagcctca tctagacacg 480
gaatccaaaa gaagctcaaa aggggtggatc aggttcctca aaagaaagat gactcaactt 540
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ggaaaggctg attacggaaa tgtacacggt ggcccgaat t 1541

<210> 308
<211> 416
<212> DNA

200/292

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(416)

<223> 3' terminal sequence. v-myb avian
myeloblastosis viral oncogene homolog -like 2
(MYBL2) gene.

<400> 308

gttannncnan tnnatTTTTT aagagagagg caatTTTatt cttccaaaaa aatgcaccag 60
agagggtgag cacaggagca cccctggcca catcccccat cctaagcagg gtctgagatg 120
aggccaggnc tgacgtgggc ttgggagaag ctgacggagc tccctgtggc cttggggagg 180
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ggcttcggca acagggcagc acatggccct gtcccttcca cctgagagt c tggggagggg 300
ctggtggcag aaggctccct gcaggagggt cacctgaatg actctcagat tcacagaccc 360
cctnttgccc ccacaacccc tgtaaaccatg agaatggggc tcgtgacacc ctnaac 416

<210> 309

<211> 426

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(426)

<223> 5' terminal sequence. v-myb avian
myeloblastosis viral oncogene homolog -like 2
(MYBL2) gene.

<400> 309

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cggacccatt caagaaagtc cggaagtctc tggctcttga cattgtggat gaggatatga 120
agctgatgat gtccacactg cccaagtctc tatccttgcc gacaactgcc ccttcaaact 180
cttcagcct caccctgtca ggtatcaaag aagacaacag cttgctcaac cagggttct 240
tgcaggcaa gcccgagaag gcagcagtgg ccagaagcc ccgaagc cac ttcacgacac 300
ctgcccctat gtccagtgc tgggaagacg gtggcctgcg gggggaccag gggaccagct 360
tttcatggca ggagaaagcc cggcagcttc tggggccgct tgaagcccag ccacactttt 420
cgggac 426

<210> 310

<211> 2627

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2627)

<223> v-myb avian myeloblastosis viral oncogene
homolog-like 2 (MYBL2) gene.

<400> 310

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<210> 311

<211> 442

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(442)

<223> 3' terminal sequence. transforming growth
factor, beta receptor iii (betaglyc an, 300kd)

202/292

(TGFB3) gene.

<400> 311

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cccagactca aggagttagt aaagggttaa tagccagata gtagaaccag tgaggagatg 60
cggccaaaga ttctttatat ctgaaccaag atgtaaaaca agaaatgctt tgaggctttc 120
taagcgatcc tcctgtctaa tttgcacctt tgtctggatg cacacttctg acctgtctgc 180
cacaacctgt ggggttctga tgtgtccctt gatgggtgct gccctcaggg actgcaccct 240
gacaagtgtt aaggcaacat tcctttcttg tgcccggggc caaaaccaat gctgatgacc 300
ttatcagctt cctgtttctt ccatacttg catacaccac tggcaaatg tcttaatggc 360
aaattttcta tttcttacag ggnctacagg aaatttgaaa atgg accaaa ttcagggaac 420
cacaggtttt gtggccatt tc 442
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<210> 312

<211> 315

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(315)

<223> 5' terminal sequence. transforming growth
factor, beta receptor iii (betaglycan, 300kd)
(TGFB3) gene.

<400> 312

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tggtgacact attcagataa ccaactggag accgacagat ttgccatgca ttgcatctt 240
gctagagttt ggtttttatg aaagggccta ttttttttta agttgacata ttttgagtgg 300
gaaacactca cccta 315
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<210> 313

<211> 4208

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4208)

<223> transforming growth factor, beta receptor
iii (betaglycan, 300kd) (TGFB3) gene.

<400> 313

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gaaagaaccg catgagcctg acggcgcctg gtcttaacat caggctgtgc aggaagaagc 120
tatctgcaga tggatgccag cacacacaag gaagcagagc tctggcaaca ttgagtcaaa 180
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ggtgcactgt gtgaactgtc acctgtcagt gcctcccatc ctgtccaggc cttgatggag 480
agcttcactg tttgtcagg ctgtgccagc agaggcaca ctgggctgcc acaggaggtg 540
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203/292

catgtcctga atctcgcact gcgccagggg cctggccagc tacagagaga ggtcacactt 600
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gatatttcca ggagagtctg gaatgaagag ggagaagatg ggctccctcg gccaaaggac 1620
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agcgtggata ttgcccgtgc tgtcaaatg t gacaatgaga agatgatcgt ggctgtagaa 1740
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tgcaaggcca agatgaatgg cacacacttt gttttggagt ctctctgaa tggctgcggt 1860
actcgcccc ggtggtcagc ccttgatggt gtggtctact ataactccat tgtgatacag 1920
gttccagccc ttggggacag tagtggttgg ccagatggtt atgaagatct ggagtcaggt 1980
gataatggat ttccgggaga tatggatgaa ggagatgctt ccctgttcac ccgacctgaa 2040
atcgtggtgt ttaattgcag ccttcagcag gtgaggaacc ccagcagctt ccaggaacag 2100
ccccacgaa acatcacctt caacatggag ctatacaaca ct gacctctt tttggtgcc 2160
tcccaggcgc tottctctgt gccagagaat ggacacgttt atgttgaggt atctgttact 2220
aaggtgaac aagaactggg atttgccatc caacgtgct ttatctctcc atattcgaac 2280
cctgatagga tgtctcatta caccattatt gagaatattt gtctaaaga tgaatctgtg 2340
aaattctaca gtcccaa gag agtgcacttc cctatccgc aagctgacat ggataagaag 2400
cgattcagct ttgtcttcaa gcctgtcttc aacacctcac tgcctttct acagtgtgag 2460
ctgacgctgt gtacgaagat ggagaagcac cccagaagt tgcctaagt tgtgcctct 2520
gacgaagcct gcacctcgt ggacgcctcg ataactggg ccatgatgca gaataa gaag 2580
acgttcacca agcccttgc tgtgatccac catgaagcag aatctaaaga aaaaggtcca 2640
agcatgaagg aaccaaactc aatttctcca ccaatttctc atggtctgga caccctaacc 2700
gtgatgggca ttgcgtttgc agcctttgtg atcggagcac tctgacggg ggcttgtgg 2760
tacatctatt ctacacaggg ggagacagca ggaaggcagc aagtcccccac ctccccgcca 2820
gcctcggaac acagcagtgc tgcccacagc atcggcagca cgcagagcac gccttgtctc 2880
agcagcagca cggcctagcc caaccaggc ccaaccggc ccaaccagc ccagccagc 2940
tcagctcagc tactccaagg gcaggaccaa tggctgagcc tegtgtccag actcagaggg 3000
ctggattttg gttcccttgt aaagacagag tgaatttcag tataaagatc acccggtgta 3060
ttcaccacac acccagggct agtataaaca tgacctggg cttctgtacc aactagaat 3120
tcatgtgaga aagctaaaat ggtgtcttc tccaccagcc cctcacagc ttgggggttt 3180
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atttggggcc ctgagtttta ccgagactca aggagttggt aaagggttaa tagccagata 3300
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agaaatgctt tgaggcttcc taagcgatcc tctgtctaa ttgcacctt tgtctggatg 3420
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ccctcaggga ctgcacctg acaagtgtta aggcaacatt ccttgcctgt gccctgggccc 3540
aaaaccaatg ctgatgacct tatcagcttc ctgtttcttc ccatactgca tacaccactg 3600
caaaatgtct taatgcaaat tttgtatttc ttacaggcct acagaaatg aaaatgac ca 3660
aaatcaggaa ccacagattt gtgcccattc ctaatatattt gttctgcaaa ttaatgtata 3720
atttgagtg aaattcagtt ataaagtcaa ggacgaattt gcacagtgt atatttctat 3780
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agagaaaatt tgaaaatgtc cttatgcttt ta gagttgca acttaagtat atttggtagg 3900
gtgagtggtt ccactcaaaa tatgtcaact taataaaaaa taggcccctt cataaaaaacc 3960
aaactgtagc aagatgcaaa tgcatggcaa atctgtcggc ctccagttgg ttatctgaat 4020
agtgtacca attccaccaa gacagtgtg agattggaaa gggcactcat ttggattgcc 4080
ttacttctct tgccttaaat atatcccata tatttaatat gtcaaaaagg gcttgaggtg 4140
aatttcatta aatggaataa tatgatgcca ctttgcagct aaaataagct cagtataacc 4200

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tccttggt

4208

<210> 314
<211> 468
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(468)
<223> 3' terminal sequence. peroxiredoxin 2
(PRDX2) gene.

<400> 314
tnnttttttt tttncacott tccctaatac ttnatnggtn acctctaggc ctgtgtgcgg 60
ctgggtgggc ttgggggagg gcgtcactat tcagcttcta ggtggaggca tgagaaggcc 120
ttggctaggc cctccagggt cccatactgt ggagtttga ggggcaggtc tggcctttcc 180
tgggtcagca tagggcaccc aggtgggggn acaggtggac acccagcaca ggcacctagg 240
caggggcaca agctcantat ccnttagcca gcctaattgt ntttgg agaa atattccttg 300
ctgtcatcca cgttgggttt aatcgtgtca ctgccaggtt tccagccagc gggacaaant 360
ttcccatgt tcgtttgtgt attgggaagg cctgggacca gccgcagagt tnatcccacg 420
gagngtccca aaggnaaatc attaaacagt gattttggcn aaggaaaa 468

<210> 315
<211> 394
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(394)
<223> 5' terminal sequence. peroxiredoxin 2
(PRDX2) gene.

<400> 315
acttcaaggc cacagcgggtg gttgatggcg ccttcaaaga ggtga agctg tcggactaca 60
aagggaagta cgtggtcctc tttttctacc ctctggactt cacttttgtg tgccccaccg 120
agatcatcgc gttcagcaac cgtgcagagg acttccgcaa gctgggctgt gaagtgtctg 180
gcgtctcggg tggactctca gttcaccac ctggcttga tcaacacccc ccggaaagag 240
ggaggcttgg gccccctgaa catc cccctg cttgctgacg tgaccagacg cttgtctgag 300
gattacggcg tgctgaaaac agatgagggc attgctaaca ggggcctctt tatcatcgat 360
gggcaagggt gttcctttcg ccagatcaat gtta 394

<210> 316
<211> 937
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>

205/292

<221> misc_feature

<222> (1)..(937)

<223> peroxiredoxin 2 (PRDX2) gene.

<400> 316

```
cgcgggcccca gggctcactt ggcgtgaga acgcgggtgc agcgtgtgat cgtccgtgcg 60
tctagccttt gccacgcag ctttcagtca tggcctccgg taacgcg cgc atcggaagc 120
cagcccctga cttcaaggcc acagcgttg ttgatggcg cttcaaagag gtgaagctgt 180
cggactacaa aggggaagtac gtggctcctt tttctaccc tctggacttc acttttgtgt 240
gccccaccga gatcatcgcg ttcacaaccg tgaagaggac ttccgcaaag ctgggctgtg 300
aagtgtctggg cgtctcgtg gactc tcagt tcaaccacct ggcttggatc aacaccccc 360
ggaaagaggg aggcttgggc cccttgaaca tccccctgct tgctgacgtg accagacgct 420
tgtctgagga ttacggcggtg ctgaaaaacg atgagggcgt tgcttacagg ggcctcttta 480
tcatcgatgg caagggtgtc cttcgccaga tcactgttaa tgatttcct gtgggacgct 540
ccgtggatga ggctctgcgg ctgggtccagg cttccagta cacagacgag catggggaag 600
tttgtccggc tgcttgggaag cctggacgtg acacgattaa gccgaacgtg gatgacagca 660
aggaatattt ctccaaacac aattaggctg gctaaccgat agtgagcttg tgcccctgcc 720
taggtgcctg tgctgggtgt ccacctgtgc cccacctgg gtgcc ctatg ctgacccagg 780
aaaggccaga cctgccccctc caaaatccac agtatgggac cctggagggc tagcaaggcc 840
ttctcatgcc tccacctaga agctgaatag tgacgcccct ccccaagccc accagccgc 900
acacaggcct agaggttaacc aataaagtat tagggcc 937
```

<210> 317

<211> 451

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(451)

<223> 5' terminal sequence. v-fos fbj murine
osteosarcoma viral oncogene homolog (FOS) gene.

<400> 317

```
gctagcacca tgagctgaag accgagccct ttgatgactt cctgttccca gcatcatcca 60
ggcccagtgg ctctgagaca gccgcgtccg tgccagacat ggacctatct gggtccttct 120
atgcagcaga ctgggagcct ctgcacagtg gctccctggg gatggggccc atggcacagn 180
agctggagcc cctgtgcaact ccggtggtca cctgtactcc cagctgcaact gctta cacgt 240
cttccttcgt cttcacctac cccgaggctg actncttccc cagctgtgca gctgcccacc 300
gcaaggcagc agcagcaatg agccttctc tgactcgttc agctnaccca cgggtgctggc 360
cctgtgaggg ggcaggggaa ggggaggcag ncggcaacna caagttgcca ttgtccgagt 420
tngttgattt anagagagga gaaacaaatt t 451
```

<210> 318

<211> 2084

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2084)

<223> v-fos fbj murine osteosarcoma viral oncogene
homolog (FOS) gene.

<400> 318
aaccgcatct gcagcgagca actgagaagc caagactgag ccggcggccg cggcgcagcg 60
aacgagcagt gaccgtgctc ctaccagct ctgcttcaca gcgccacct gtctccgcc 120
ctcgccctt cgcccggctt tgcctaaccg ccacgatgat gttctcgggc ttaacgcag 180
actacgagcg gtcctcctcc cgctgcagca gcgcgtcccc ggccggggat agcctctctt 240
actaccactc acccgagac tccttctcca gcatgggctc gcctgtcaac gcgcaggact 300
tgtgcacgga cctggccgtc tccagtcca acttcattcc caccgtcact gccatctcga 360
ccagtcggga cctgcagtgg ctggtgcagc ccgcctcgt ctctctgtg gccccatc gc 420
agaccagagc ccctcaccct ttccggagtc ccgccccctc cgctggggct tactccaggg 480
ctggcggtgt gaagaccatg acaggaggcc gagcgagag cattggcagg aggggcaagg 540
tggaacagtt atctccagaa gaagaagaga aaaggagaat ccgaaggaa aggaataaga 600
tggctgcagc caaatgccg aaccggagga gggagc tgac tgatacactc caagcggaga 660
cagaccaact agaagatgag aagtctgctt tgcagaccga gattgccaac ctgctgaagg 720
agaaggaaaa actagagttc atcctggcag ctaccgacc tgctgcaag atccctgatg 780
acctgggctt ccagagaag atgtctgtgg ctcccttga tctgactggg ggctgccag 840
aggttgccac ccgaggtct gaggaggcct tcacctgcc tctctcaat gacctgagc 900
ccaagccctc agtgaacct gtcaagagca tcagcagcat ggagctgaag accgagccct 960
ttgatgactt cctgttcca gcatcatcca ggccagtggt ctctgagaca gcccgctccg 1020
tgccagacat ggacctatct gggctcttct atgcagcaga ctgggagcct ctgca cagtg 1080
gtccctggg gatggggccc atggccacag agctggagcc cctgtgact ccggtggtca 1140
cctgtactcc cagctgact gcttacagt ctctctctg ctccacctac ccgaggctg 1200
actccttccc cagctgtgca gctgccacc gcaagggcag cagcagcaat ggccttctc 1260
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ccggcaccac caagtgcac tgcccagct ggtgcattac agagaggaga aacacatctt 1380
cctagagggg ttcctgtaga cctaggagg accttatctg tgcgtgaaac acaccaggct 1440
gtgggcctca aggacttgaa agcatccatg tgtggactca agtccttacc tctccggag 1500
atgtagcaaa acgcatggag tgtgtattgt tcccagtgc acttcagaga gctggtagtt 1560
agtagcatgt tgagccaggc ctgggtotgt gtctctttt tctttctct tagtcttctc 1620
atagcattaa ctaatctatt gggttcatta ttggaattaa cctgggtctg gatattttca 1680
aattgtatct agtgcagctg attttaacaa taactactgt gtt cctggca atagtgtgtt 1740
ctgattagaa atgaccaata ttatactaag aaaagatacg actttatttt ctggtagata 1800
gaaataaata gctatatcca tgtactgtag tttttcttca acatcaatgt tcattgtaat 1860
gttactgac atgcattgtt gaggtggtct gaattgtctg acattaacag ttttccatga 1920
aaacgtttta ttgtgtttt aatttattta ttaagatgga ttctcagata tttatatttt 1980
tattttattt ttttctacct tgaggtcttt tgacatgtgg aaagtgaatt tgaatgaaa 2040
atthaagcat tgtttgctta ttgtccaag acattgtcaa taaa 2084

<210> 319

<211> 240

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(240)

<223> 3' terminal sequence. retinoblastoma -binding
protein 7 (RBBP7) gene.

<400> 319

ctgcaaagcc aatcaagaag tgttgaagg aaaaagtgt aaagttattc ttgcatattt 60
gggaacagca agcacttagt ttgagaaaat gaggacttaa aacagttgan tcaaaggcaa 120
taccctgcta cttgtattta aaatcaatgg tgatgttatt tcttangcaa cattcttctc 180
ttccctaata gctacaatnt gatacagtac gcaacagctc acttgaaagt gctagantca 240

<210> 320

207/292

<211> 457

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(457)

<223> 5' terminal sequence. retinoblastoma -binding protein 7 (RBBP7) gene.

<400> 320

```
agatgtttga agatactgtg gaggagcgtg tcatcaatga agaatat aaa atctggaaga 60
agaatacacc gtttctatat gacctgggta tgacccatgc tcttcagtgg ccagtcctta 120
ccgttcagtg gcttcctgaa gtgactaaac ctgaaggaaa agattatgcc cttcattggc 180
tagtgctggg gactcatcacg tctgatgagc agaatcatct ggtgggttgc cgagtacata 240
ttcccaatga tgatgcacag tttgat gctt cccattgtga cagtgacaag ggtgaatttg 300
gtggcttttg ttctgtaaca ggnaaaattg aatgtgaaat taaaatcaat tcacgaagga 360
gaagttaaac cgtgctcggt aacatggccg cagantcctt cacatccatt gcttacaaan 420
acacctctt gcttgatggt gttggnnttt tgactat 457
```

<210> 321

<211> 1946

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1946)

<223> retinoblastoma -binding protein 7 (RBBP7) gene.

<400> 321

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gcctcgtcag ctgcctgggc gggc tgggag gcgcggggtg aaaagtctcg ttccaagttt 60
ggagagagag agaagagcgc ctacagacctc ggtacccgcg agcggggagg aggcaggaaa 120
gaaggacgcg gcgtctgggg agcaccagg cagcaagacg gggcccgggc ttctgacagt 180
ggggagtgtg acgcgcttgg gaaaggcagg agcgccagcg gtcgggctgc tcttggttaa 240
cgagaggagt ccgaggcggc ggcgaggggc gaacgacctg acgcaagatg gcgagtaaag 300
agatgtttga agatactgtg gaggagcgtg tcatcaatga agaataaaa atctggaaga 360
agaatacacc gtttctatat gacctgggta tgacccatgc tcttcagtgg ccagtcctta 420
ccgttcagtg gcttcctgaa gtgactaaac ctgaaggaaa agatt atgcc cttcattggc 480
tagtgctggg gactcatcac tctgatgagc agaatcatct ggtgggttgc cgagtacata 540
ttcccaatga tgatgcacag tttgatgctt cccattgtga cagtgacaag ggtgaatttg 600
gtggcttttg ttctgtaaca ggaaaaattg aatgtgaaat taaaatcaat cacgaaggag 660
aagtaaaccg tgctcgttac atg ccgcaga atcctcacat cattgctaca aaaacaccat 720
cttctgatgt gttgggtttt gactatacaa aacacctgac taaaccagac ccaagtggag 780
aatgtaatcc tgatctcaga ttaagaggtc accagaagga aggctatggt ctctoctgga 840
attcaaattt gagtggacat ctctaagtg catctgatga ccatactgtt tgtctgtggg 900
atataaacgc aggacaaaa gaaggcaaaa ttgtggatgc taaagccatc tttactggcc 960
actcagctgt ttagaggat gtggcctggc acctgctgca cgagtcattg tttggatctg 1020
ttgctgatga tcagaaactt atgatatggg acaccaggtc caataccacc tccaagccga 1080
gtcacttggg ggatgcgcac actgccgaag tcaactgcct c tcattcaat ccctacagcg 1140
aatttattct agccaccggc tctgcggata agaccgtagc tttatgggat ctgcgtaact 1200
taaaattaaa actccatacc ttcgaatctc ataaagatga aattttocag gtccactggt 1260
ctccacataa tgaaactatt ctggcttcaa gtggtactga ccgccgcctg aatgtgtggg 1320
```


208/292

```

atttaagtaa aattggggaa gaacaatcag cagaagatgc agaagatggg cctccagaac 1380
tctgttttat tcatggagga cactactgta agatttcaga ttttagctgg aaccccaatg 1440
agccttgggt catttgctca gtgtctgagg ataacatcat gcagatatgg caaatggctg 1500
aaaatattta caatgatgaa gagtcagatg tcacgacatc cgaactggag ggaca aggat 1560
cttaaaccce aagtacgaga aatgtttctg ttgaatgtaa tgctacatga atgcttgatt 1620
tatcaagcgc caaaaaggca ttgtatagta ggaaatgtaa gtggggtggc ttatggcttc 1680
tttatcctct gattctagca ctttcaagt agctgttgcg tactgtatca tattgtagct 1740
attagggaa agagaagtgt tgcttaagaa agaacatcac cattgatttt aaatacaagt 1800
agcagggtat tgcctttgat tcaactgttt taagtcctca tttctcaaa ctaagtgtt 1860
gctgttccca aatatgcaag aataactttt acactttttc ctccaacac ttcttgattg 1920
gctttgcaga aataaagttt taaaat 1946

```

<210> 322

<211> 365

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(365)

<223> 3' terminal sequence. kiaa1075 protein
(KIAA1075) gene.

<400> 322

```

tatagaaatt ctttattatt agacaaaaat agactctctt ttttccccta ttcatgtgat 60
cctactctga atctctgctc agaggaggca gtgactcgct cccacccct ctcctatccc 120
tgccgtgctg gcacctgcag ctgggtggaa ctggcagggg ctgatccct gggagggtg 180
acgttctcct gcagggtggg ctgcctgatc tccttggggg ctcaactgct gatgcctcct 240
caccctcac acacccatct ctgccatctg ctcacatggc aagggtcatc ttgtggggcc 300
tgggtccact taacttaggc agggctgggg ggcgggggaa gggagaggca gtgttcccag 360
gggcc 365

```

<210> 323

<211> 400

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(400)

<223> 5' terminal sequence. kiaa1075 protein
(KIAA1075) gene.

<400> 323

```

tcaagggtg cccagtgag ccctactttg gcagcctgtc cgccttggtc tcccagcact 60
ccatctcccc catctcctg cctgctgccc tgcgcattcc cagcaaagat cctctggaag 120
agaccccaaga ggtccagtg cccaccaaca tgagcacagc gncagacctc ctgctcagg 180
gtgctgcctg caggtngctc tacttgacct cagtggagac agagtactg acgggcccc 240
aagctgtggc ccgggccagc tctgcagctc tgagctgta g ccccgcccg acaccagctg 300
ttgtccactt caaggtgtca gccaggga ttnacactga cgggacaacc aaaggaagct 360
cttntttttc gccgcatta tccagtggaa cagcatcacc 400

```

209/292

<210> 324
 <211> 489
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(489)
 <223> 5' terminal sequence. atp-binding cassette,
 sub-family c (cftr/mrp), member 5 (ABCC5) gene.

<400> 324
 ntctggcaca gnaagataca actctgtgct gaacagctgc tgcctgaggc tgacctggcc 60
 attcttccca gcagcgacct gacggagatt ggagagcgag tancaacctg agcgggtggc 120
 agcgcagagg atcagccttg cccgggcctt gtatagtgc aggagcatct acatcctgga 180
 cgacccctc agtgccttag atgcccattg ggaanccaca tncctcaata gtgctatccg 240
 gaaacatctc aagtccaaga cagttctggt tgttaccac cagt tacagt acctgggttg 300
 actgtgatga agtgatcttc atgaaagagg gctgtattta cgggaaagag ggcaccntg 360
 gaggaantg atggatttta aatggtgatt atggttacct ttttaattaa cntgttggtg 420
 ggggagagac accgccattg agntcatttc aaaaagggga accgtnggtt cacagaggag 480
 ttcacagt 489

<210> 325
 <211> 5838
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(5838)
 <223> atp-binding cassette, sub-family c
 (cftr/mrp), member 5 (ABCC5) gene.

<400> 325
 ccgggcaggt ggctcatgct cgggagcgtg gttgagcggc tggcgcggtt gtcttgagc 60
 aggggcgcag gaattctgat gtgaaactaa cagtctgtga gccctggaac ctccgctcag 120
 agaagatgaa ggatatcgac ataggaaaag agtatatcat cccagtcct gggatatagaa 180
 gtgtgaggga gagaaccagc acttctggga cgcacagaga ccgtgaagat tccaagtcca 240
 ggagaactcg accgttgaa tgccaagatg ctttgaaac agcagccga gccgagggcc 300
 tctctcttga tgcctccatg cattctcagc tcagaatcct ggatgaggag catcccaagg 360
 gaaagtacca tcatggcttg agtgctctga agcccatccg ga ctacttcc aaacaccagc 420
 acccagtga caatgctggg ctttttctct gtatgacttt ttctgtggctt tcttctcttg 480
 cccgtgtggc ccacaagaag ggggagctct caatggaaga cgtgtggtct ctgtccaagc 540
 acgagtcttc tgacgtgaac tgcagaagac tagagagact gtggcaagaa gagctgaatg 600
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<210> 326

<211> 385

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(385)

<223> 3' terminal sequence. cadherin 1, type 1,
e-cadherin (epithelial) (CDH1) gene.

<400> 326

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cacacatgta tacactcaaa actacagtga catt ctctac acagnnctat attcgatata 180
gottgaactg ccgaaaaatc angacaattc caaaagggtga ttgcagggtt gatttttttc 240
tccaaaacac ttgaganaca gtaaagctat ttcaacaaag gtcttttctt tgattgtcaa 300
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<210> 327

<211> 423

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(423)

<223> 5' terminal sequence. cadherin 1, typ e 1,
e-cadherin (epithelial) (CDH1) gene.

<400> 327

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<210> 328

<211> 4828

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4828)

<223> cadherin 1, type 1, e-cadherin (epithelial)
(CDH1) gene.

<400> 328

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<210> 329

<211> 471

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(471)

<223> 5' terminal sequence. zinc finger protein
144 (mel-18) (ZNF144) gene.

<400> 329

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<210> 330

<211> 2227

<212> DNA/RNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2227)

<223> zinc finger protein 144 (mel -18) (ZNF144)
gene.

<400> 330

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ggccactgga gtctcaataa agctctgcac catcctcgt gtttcccaag gcaggtgggtg 1620
tgttgggggc ccttcagac ccaaagcttt aggcattgatt ccaactggct gcatatagga 1680
gtcagttaga attgtttctt tctctcccc tttctctccc catcttggct gctgtcctgc 1740
ctctgaccag tggccgcccc ccgctgtgtt gaatgtccag aaattgctaa gaacagtgcc 1800
ttttacaaat gcagtttatc cctggttctg agggcaagt gcagggtgga ggtggcacct 1860
gcattcacct cctctcttgc agtggaact ttgtgcaaag aatagatagt tctgcctctt 1920
ttttttttt tctctgtgtg tgtggccttt gcatcattta tcttgtggaa aagaagattc 1980
aggccctgag aggtctcagc tcttgaggga gggctaaggc tttagcattg tgaagcgtg 2040
cacccccacc aaccttacc tcaccgggga accctcacta gcaggactgg tgggtggagt 2100
tcacctggg cctagagtgg aagtgggggt ggggttaacct cacacaagca cagatcccag 2160
actttgccag aggcaaacag ggaattccgc cgatactgac gggctccagg agt cgtcgcc 2220
acactcg 2227

```

<210> 331
<211> 254
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(254)
<223> 3' terminal sequence. macrophage stimulating
1 (hepatocyte growth factor -like) (MST1) gene.

<400> 331
gcataaagag gaaacatggc tttatgtctg acaagaagtt ttgtcctccc caaggcatat 60
ggcatcaagg ctgggctaac ccagtctcat gaccttgtga atccagtcca caaacacaga 120
gacacgcgtg aagacagctg gccagcggga ccttgcgcat actcggttgg ggattataat 180
tccttcacag gacccagcag ttgtgggtaa agcaggcaag tgggcccccg tagtcaccct 240
cacaggcccc caca 254

<210> 332
<211> 362
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(362)
<223> 5' terminal sequence. macrophage stimulating
1 (hepatocyte growth factor -like) (MST1) gene.

<400> 332
gccatggnc tggtgctaca cgatggaccc aaggacccca t tcgactact gtgccctgcg 60
acgctgcgct gatgaccagc cgccatcaat cctggacccc ccagaccagg tgcagtttga 120
gaagtgtggc aagagggtgg atcggctgga tcagcggcgt tccaagctgc gctggttggg 180
ggccatccgg gcaactcacc ctggacagtc agcttgcgga atcggcaggg ccagcatttc 240
tgcggnggt ctctagttaa ggagcagtn atactgactn cccggaagtg cttctcctcc 300
tncatatnc ctctcacggg ctatgaggtg tggtnnggc ancctttttc cagaaccac 360
ag 362

<210> 333
<211> 2219
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2219)
<223> macrophage stimulating 1 (hepatocyte growth
factor-like) (MST1) gene.

<400> 333

```
agccagaagg atgggggtggc tcccaactcct gctgcttctg actcaatgct taggggtccc 6 0
tgggcagcgc tgcgcattga atgacttcca agtgctocgg ggcacagagc tacagcacct 120
gctacatgcg gtggtgcccg ggccttggca ggaggatgtg gcagatgctg aagagtgtgc 180
tggtcgctgt gggcccttaa tggactgccc ggccttccac tacaacgtga gcagccatgg 240
ttgccaaactg ctgccatgga ctcaacactc gcccacacg aggtgctggc gttctggggc 300
ctgtgacctc ttccagaaga aagactacgt acggacctgc atcatgaaca atgggggttg 360
gtaccggggc accatggcca cgaccgtggg tggcctgccc tgccaggctt ggagccacaa 420
gttcccgaat gatcacaagt acacgcccac tctccggaat ggctggaag agaacttctg 480
ccgtaaccct gatggcgac c cggagggtcc ttggtgctac acaacagacc ctgctgtgcg 540
cttcagagc tgcggcatca aatcctgccc ggaggccggc tgtgtctggt gcaatggcga 600
ggaataccgc ggcgcggtag accgcacgga gtcaggggcg gactgcccagc gctgggatct 660
tcagcaccgc caccagcacc ccttcgagcc gggcaagttc ctgcaccaag gtctggacga 720
caactattgc cggaaatcctg acggctccga gcggccatgg tgctacacta cggatccgca 780
gatcgagcga gagttctgtg acctcccccg ctgcgggtcc gaggcacagc cccgccaaga 840
ggccacaact gtcagctgct tccgcgggaa gggtagggc taccggggca cagccaatac 900
caccactgcg ggcgtacctt gccagcgttg ggacgcgca a atccgcac agcaccgatt 960
tacgccagaa aaatacgcgt gcaaagacct tcgggagaac ttctgcccga accccgacgg 1020
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gatccggcgt tgtacagacg acgtgcggcc ccaggactgc taccagggcg caggggagca 1140
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gacgcgcac aagccgcagt tcacgtttac ctccgaaccg catgcacaac tggaggagaa 1260
cttctgcccg aaccagatg gggatagcca tgggccctgg tgctacacga tggacccaag 1320
gaccccatc gactactgtg ccctgcgacg ctgcgctgat gaccagccgc cat caatcct 1380
ggacccccca gaccaggtgc agtttgagaa gtgtggcaag aggggtggatc ggctggatca 1440
gcggcggttc aagctgcgcg tgggtggggg ccacccgggc aactcaccct ggacagtcag 1500
cttgcggaat cggcagggcc agcatttctg cggggggtct ctagtgaagg agcagtggtat 1560
actgactgcc cggcagtgct tctcctcc tg ccatatgcct ctacagggt atgaggtatg 1620
gttgggcacc ctgttccaga acccacagca tggagagcca agcctacagc ggggtccagt 1680
agccaagatg gtgtgtgggc cctcaggctc ccagcttgct ctgctcaagc tggagagatc 1740
tgtgacctg aaccagcgtg tggccctgat ctgcctgccc cctgaatggt atgtggtgcc 1800
tccagggacc aagtgtgaga ttgcaggctg gggtagagacc aaaggtacgg gtaatgacac 1860
agtccataat gtggccttct tgaatgttat ctccaaccag gactgtaaca tcaagcaccg 1920
aggacgtgtg cgggagagtg agatgtgcac tgagggactg ttggccctg tgggggctg 1980
tgagggtgac tacgggggcc cacttgctct ctttaccac a actgctggg tcttggagg 2040
aattataatc cccaaccgag tatgcgcaag gtcccgtg ccagctgtct tcacgcgtgt 2100
ctctgtgttt gtggactgga ttcacaaggc catgagactg ggttaggccc agccttgatg 2160
ccatatgcct tggggaggac aaaacttctt gtcagacata aagccatgtt tctcttta 2219
```

<210> 334

<211> 431

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(431)

<223> 3' terminal sequence. glutathione
s-transferase pi (GSTP1) gene.

<400> 334

```
gaaaggaagg caaactctgc ccccc gctca gagtcccccc aaccctcact gtttcccggt 60
gccattgatg gggaggttca cgtactcagg ggaggccagg naggcntgna gcttggggccg 120
ggcactgagg cgcgccacat atgctgagag cagggggaac gcatccaggc agccagggct 180
agggaccnca tggatcagca gcaagtccag caggttntag tcagcgaagg agntctggtc 240
tcccacaatg aaggtcttgc ctccctggtt ctgggacagc aggttctcaa aaggtcttcg 300
```

217/292

ttgcccgggc agtgccttca catagtcato cttgcccgcc tcatagttgg tntagatgag 360
ggagatgtat ttgcagcgga ggtcctccac gccgttcatt tcacctgtcc accagggtg 420
nctcctttt t 431

<210> 335
<211> 305
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(305)
<223> 5' terminal sequence. glutathione
s-transferase pi (GSTP1) gene.

<400> 335
nattcggcac aggtcgccac catgccgccc tacaccgtgg tctatttccc agttcgaggc 60
cgctgcctgt cggcaatgct gctggcagat cagggccaga gctggaagga ggaggtngtg 120
accgtggaga cgtggcagga gggctcactc aaagcctcct gcctatacgg gcagctcccc 180
aagttccagg acggagacct naccctgtac cagt ccaata ccacctgcg tcacctgggc 240
cgcacccttg ggctnctatg ggaaggacca gcaggangca gccctggtgg acatngtgaa 300
tgacg 305

<210> 336
<211> 737
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(737)
<223> glutathione s-transferase pi (GSTP1) gene.

<400> 336
ggagtttcgc cgcgcagtc ttgccacca tgccgccta caccgtggtc tatttcccag 60
ttcgaggccg ctgcgcggcc ctgcgcatgc tgctggcaga tcagg gccag agctggaagg 120
aggagggtgt gaccgtggag acgtggcagg agggctcact caaagcctcc tgcctatacg 180
ggcagctccc caagttccag gacggagacc tcaccctgta ccagtccaat accatcctgc 240
gtcacctggg ccgcaccctt gggctctatg ggaaggacca gcaggaggca gccctggtgg 300
acatggtgaa tgacggcgtg gag gacctcc gctgcaaata catctccctc atctacacca 360
actatgaggc gggcaaggat gactatgtga aggcactgcc cgggcaactg aagccttttg 420
agaccctgct gtcccagaac cagggaggca agaccttcat tgtgggagac cagatctcct 480
tcgtgacta caacctgctg gacttgctgc tgatccatga ggtcctagcc cctggctgcc 540
tgatgctgtt cccctgctc tcagcatatg tggggcgcct cagcgcccg cccaagctca 600
aggccttcc tggcctccct gagtacgtga acctcccat caatggaac gggaaacagt 660
gagggttggg gggactctga gcgggaggca gagtttgcct tcctttctcc aggaccaata 720
aaatttctaa gagagct 737

<210> 337
<211> 372
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(372)

<223> 3' terminal sequence. b-cell cll/lymphoma 2
(BCL2) gene.

<400> 337

```
gtgggnctgt gttgaaacag gccacgtaaa gcaactctct aaaggtcaaa ccaccataga 60
tttgaatctg ctgggtcattc gccatctgga tttttaactg aatgaatctc atgggtttta 120
ccaaacatgc atgtaatcct gaataccatg anttaaagtc gganttgccc agggacgagg 180
aaaccttcaa gaaacaaggt caaagggaca ncagatata a ctgtcacant aaacanttct 240
gttgacgtgg gaaatgcaca tgacttggtt gaaacaaagc tcctcagtgg gccagtga 300
tcnngggttt ttcttagggt aggctgagga ctcaggggct tatctcacct tctcaggaat 360
gctttttgaa gg                                     372
```

<210> 338

<211> 508

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(508)

<223> 5' terminal sequence. b-cell cll/lymphoma 2
(BCL2) gene.

<400> 338

```
nttcggcaca gacttttttt aagctaccaa ttg tgccgag aaaagcattt tagcaattta 60
tacaatatca tccagtacct taaaccctga ttgtgtatat tcatatattt tggatacgca 120
ccccccaact cccaatactg gctctgtctg agtaagaaac agaatcctct ggaacttgag 180
gaagtgaaca tttcgggtgac ttccgcatca ggaaggctag agttaccagc agcatcaggc 240
cgccacaagt gcctgctttt aggagaccga agtcgcgcaga acctgcctgt gtcccagctt 300
ggaggcctgg gtccctggga ctgagccggg gccctcactg gccttccttc caggggatgg 360
atcaacaggg gcagtgtggt cttccgaatg tctgggaagc tgatgggagc tcagantttc 420
cactgtcaag aaagaggcag ttaggagggg tttgggtggg gcttggtcac ctgg ggggcc 480
ttccaggtag ggcccttttt aagtggga                                     508
```

<210> 339

<211> 445

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(445)

<223> 3' terminal sequence. proliferating cell
nuclear antigen (PCNA) gene.

<400> 339

219/292

```
tttttttant caaaagtgtg aaattcaagt aactttattt aaattcaaaa acaattctta 60
aaactgcatt tagagtcaag acccttttgt attataaaaa tcacaagtat ttctaagaga 120
caaaaatact tctaggttaa ctagaccaga tctgactt tg gactttattc tttaaacaan 180
ttgcagagan tagagaaaaa antagggtat ttacagaaaa caatatctac atatgtactt 240
ngnggtacaa ntttgggtga cagaaaagac ttcaggtata tgctgggcat cttagggaagn 300
cagttctcaa agggnccttag gttttatttn cttggatttt taaggattgc cctaagganc 360
ccttcttcat cctcgn tctt gggggngggc aggtaggtnt tttaggtgtc ccntatccc 420
ganttttata ctctncaccg ggggg                                     445
```

<210> 340

<211> 437

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(437)

<223> 5' terminal sequence. proliferating cell
nuclear antigen (PCNA) gene.

<400> 340

```
gctccagcgt tgtaaacctg cagagatgga ctggtccac gtctctttgg tgcagctcac 60
ctgcggtct gagggcttcg acacctaccg ctgcgaccgc aacctggcca tggggtgaac 120
ctcaccagta tgtccaaaat actaaaatgc gccggcaatg aagatatcat tacactaagg 180
gccgaagata acgcggatac cttggcgcta gtatttgaag caccaaacca ggagaaagtt 240
tcagactatg aaatgaagtt gatggattta gatgttgaac aacttngaag tccagaacag 300
gagtacagct gtgtagtaaa gatgcctct ggtgaatttg c acgtatatg ccgagatctc 360
agccatattg ggagatgctg ttgtaatttc ctgtgncaaa agacgggagt gaaaattttt 420
ctgcaagtgg gagnact                                     437
```

<210> 341

<211> 1231

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1231)

<223> proliferating cell nuclear antigen (PCNA)
gene.

<400> 341

```
aggcttcagc cggctcgtgc gacgttcgcc cgctcgtct gaggtcctg aagccgaaac 60
tagctagact ttctctcttc ccgcctgct gttagcggct tggtgccact ccgccacat 120
gttcgaggcg cgcctggtcc agggctccat cctcaagaag gtgttgagg cactcaagga 180
cctcatcaac gaggcctgct gggatattag ctccagcggg gtaaacctgc agagcatgga 240
ctcgtccac gtctctttgg tgcagctcac cctgcggtct gagggcttcg acacctaccg 300
ctgcgaccgc aacctggc ca tgggogtgaa cctcaccagt atgtccaaa tactaaaatg 360
cgccggcaat gaagatatca ttacactaag ggccgaagat aacgcggata ccttggcgct 420
agtatttgaa gcaccaaacc aggagaaagt ttcagactat gaaatgaagt tgatggattt 480
agatgttgaa caacttgaa ttccagaaca ggagtacagc tgtgtagtaa agatgccttc 540
tggtgaattt gcacgtatat gccgagatct cagccatatt ggagatgctg ttgtaatttc 600
ctgtgcaaaa gacggagtga aattttctgc aagtggagaa cttggaaatg gaaacattaa 660
```

220/292

```

attgtcacag acaagtaatg tcgataaaga ggaggaagct gttaccatag agatgaatga 720
accagttcaa ctaacttttg cactgaggta cctgaact tc ttacaaaag ccactccact 780
cttttcaacg gtgacactca gtatgtctgc agatgtaccc cttgttgtag agtataaaat 840
tgcggatatt ggacacttaa aatactactt ggctcccaag atcgaggatg aagaaggatc 900
ttaggcattc ttaaaattca agaaaataaa actaagctct ttgagaactg cttctaagat 960
gccagcatat actgaa gtct tttctgtcac caaatttgta cctctaagta catatgtaga 1020
tattgttttc tgtaaataac ctattttttt tctctattct ctccaatttg tttaaagaat 1080
aaagtccaaa gtctgatctg gtctagttaa cctagaagta tttttgtctc ttagaaatac 1140
ttgtgatttt tataatacaa aagggtcttg actctaaatg cagttttaag aagtg ttttt 1200
gaattttaat aaagttactt gaatttcaaa c                                     1231

```

<210> 342

<211> 383

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(383)

<223> 3' terminal sequence. adenovirus 5 ela
binding protein (BS69) gene.

<400> 342

```

tttttttttt aaacacacan gttttcacgc tgtagtaact tggaaatgtg caaccctgtg 60
caacagagac agaaaagcca aagtaacacg aatctcactt tcatgcagct atcagttaaa 120
tattacatac tctggaatga ttttacacca aaaatattt c cacaattact tgcttcata 180
ggggtggatc gaagtcttaa aacttgaaaa acaatcaaag aagggttaagt gttctcgggt 240
ctgacatctc catcagcgcc acacactgtg gngaacactg gactaattac acagcaacaa 300
ggagggggaac gatgatgcca agttactgca taatttaggg tacattgtat ggaatggggg 360
gctactgggg gtactttttt tac                                     383

```

<210> 343

<211> 483

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(483)

<223> 5' terminal sequence. adenovirus 5 ela
binding protein (BS69) gene.

<400> 343

```

gttnaaattg cagggactgg ggtaatcttt tactgagctg gatcttagag aaaatgaata 60
tttaaatttt aaagtttgca catttcactt ttgtcctaac atgagtgtt gtaacaaaat 120
aaacaacaaa aacaaagcca aaaactacct ttatccatat gtgaaattat agatgaggca 180
tacgaatttg tttaatgctt ccttccctt ccacatac atctcactgc ctattatctg 240
gtgtcacctc atgtatcgta agttaatact aaaagaagag aaagcactta agtttcacag 300
aagccgttat gttttagagt aatgggtgca ttgcctaagt gaactccatc actgtacaca 360
gaatgaagga nttaatgcca tgtaatttt cttgttattt aagg atgccg tggatttggt 420
aaaaggctctg gtattttgcy gggatgtctg gggtaggga ggccttacc ataggggntg 480
ggg                                     483

```

<210> 344
<211> 2722
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2722)
<223> adenovirus 5 ela binding protein (BS69)
gene.

<400> 344
ggagcataat gctaaagaag taaacaggtc atggcacgtt taacaaaaag acgacaggcg 60
atacaaaagc tatccagcat ctttgggcag ccattgagat tata cggaac cagaagcaga 120
ttgccaaat tgaccgtatt acaaaatgtg aaacaactac attattcttg aacctatggt 180
gatttttaca tcattacaca gatattgcat tttcattagt tgtatcattg ttataaactg 240
gtatattgct cgagttccag gtatgcacc taaagagacc acccgtcagc tgagcttagc 300
tgtgaaagat ggtcttattg tc gaaactct aacagtgggc tgcaaaaggtt caaaagctgg 360
tattgaacaa gaaggatatt ggttgccagg agatgagatt gactgggaaa cagaaaaatca 420
tgactggtat tgttttgaat gccatttgcc tggagaggtg ttgatattgt acctgtgttt 480
tcgtgtgtat cattccaagt gtttgtctga tgagttcagg cttagagaca gcagtagtcc 540
ctggcagtg ccagtttgca ggagcattaa gaagaagaat acaacaaaac aggagatggg 600
cacatacctc agattcattg tctcccgcat gaaggagagg gctatagatc ttaataaaaa 660
ggggaaggac aataaacacc cgatgtacag gaggtggtg cactcagctg tggacgttcc 720
caccattcaa gagaaagtga atgaaggga ataccgaagt ta tgaagagt tcaaagctga 780
tgcccaattg cttctccaca ataccgtgat ttctatgga gcagacagtg agcaagctga 840
cattgcgagg atgctatata aagacacatg tcatgagctg gatgaactgc agctttgcaa 900
gaattgcttt tacttgtaa atgctcgtcc tgacaactgg ttctgttatc cttgtatacc 960
taatcatgag ctggtttggg ctaaaatgaa aggttttggg ttttggccag ccaaagtcac 1020
gcagaaagaa gacaatcaag tcgacgttcg cttctttggc caccaccacc agagggcctg 1080
gattccttct gaaaacattc aagatatac agtcaacatt catcggtcgc acgtgaagcg 1140
cagtattggg tggaaaaagg cctgtgatga gctggagctg catcagcgtt tcctacgaga 1200
aggagatatt tggaaatcta agaattgagga ccgaggtgag gaagaggcag aatccagtat 1260
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acgtaatcaa agtgtggagc ccaaaaagga agaaccagag cctgaaacag aagcagtaag 1380
ttctagccag gaaataccca cgatgcctca gccc atcgaa aaagtctccg tgtcaactca 1440
gacaaaagag ttaagtgcct cttaccaag aatgctgcat cggagcacc agaccacaaa 1500
cgacggcgtg tgtcagagca tgtgcatga caaatacacc aagatcttca atgacttcaa 1560
agaccggatg aagtccgacc acaagcggga gacagagcgt gttgtccgag aagctctgga 1620
gaagctgcgt tctgaaatgg aagaagaaa gagacaagct gtaaataaag ctgtagccaa 1680
catgcagggt gagatggaca gaaaatgtaa gcaagtaaag gaaaagtgt aggaggaatt 1740
tgtagaagaa atcaagaagc tggcaacaca gcacaagcaa ctgatttctc agaccaagaa 1800
gaagcagtgg tgctacaact gtgaggagga ggccatgtac cactgctg ct ggaacacatc 1860
ctactgctcc atcaagtgcc agcaggagca ctggcacgcg gacacaagc gcacctgccg 1920
ccgaaaaaga tgaagctggc ccttcccgga gtcaaccgga tgattactct tttcagacac 1980
agcggttttt gtttccaaga agccaaaatt gtttagaatt tgcttcccat tttgaccag 2040
cctttaaaca ctttctgtga ag aaattttg cacagtagtt taaatctttt gttaatgctc 2100
ctccgaagtt tttcaggggg taaaagtaac atcagtgag ggtattattt taaataaatt 2160
ttaattgaga atttgttgca tttcagcaa attttaaac atttttaggt tttacagaga 2220
ttttaacctt taaacaacag atctttaaaa aacaggtgaa tacaagttag tttacaaaag 2 280
aaacatttag atagatctg aatgtaagaa ctacagaact gtttcagaaa taaaacatac 2340
taccttgatg tgacattttt ttcttaacct tgttgagctg gttttgttca gcttaattta 2400
ctgttcaaag gcattatctg ttggtcacac cagtgggtat atgattgaat ttagggaaca 2460
gggttgacac agcagggcta gtctgcata tttttt ctta aatatttccc aattgtgttt 2520
ttcattattt cttttcaata tataactttt ataacaaatt attagctttg atctttagt 2580
ttaaaattgc agggaactgg ggtaatcttt tactgagctg gatcttagag aaaatgaata 2640
tttaaatttt aaagtttgcc acatttcatc tttgtcctaa catgagtgtc tgtaacaaaa 2700

222/292

taaaacaaca aaaacaaagc ct

2722

<210> 345

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(363)

<223> 3' terminal sequence. matrix
metalloproteinase 11 (stromelysin 3) (MMP11) gene.

<400> 345

```
gcattgcagca tcctgagtgg tagcgtcgat ctcagagggc acccctctcc agtcagtggc 60
cctgcgggna cggngactgt ctacacgccg ggtgctgggg tggaaacgcc agtagtcctt 120
gcctcggaag aagtagatct tggtcttctc gggacccacg accaaggc ag catggaccgg 180
gaacctcacc agggcccagc tcggtgaggg gtgcggggcc cagggactgg cttttcaccg 240
tcgtacaccc agtacttgag caccttggga agaaccaaaat gtgggcccgg cttaccacgc 300
attggccttt tcgccacagg gctggggcag tccctgccag tngcgagaag ccaatttttg 360
gca                                     363
```

<210> 346

<211> 2260

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2260)

<223> matrix metalloproteinase 11 (stromelysin 3)
(MMP11) gene.

<400> 346

```
aagcccagca gcccgggggc ggatggctcc ggccgcctgg ctccgcagcg cggccgcgcg 60
cgccctcctg ccccgatgc tgctgctgct gctccagccg ccgcccgtgc tggcccgggc 120
tgtgccgccc gacgtccacc acctccatgc cgagaggagg gggccacagc cctggcatgc 180
agccctgccc agtagcccgg cacctgcccc tgccacgcag gaagcccccc ggcctgccag 240
cagcctcagg cctccccgct gtggcgtgcc cgacccatct gatgggctga gtgcccgcaa 300
ccgacagaag aggttcgtgc tttctggcgg gcgctgggag aagacggacc tcacctacag 360
gatccttcgg ttcccattgg agttggtgca ggagcaggtg cggcagacga tggcaga ggc 420
cctaaaggta tggagcgatg tgacgccact cacctttact gaggtgcacg agggccgtgc 480
tgacatcatg atcgacttgc ccaggtactg gcatggggac gacctgccgt ttgatggggc 540
tgggggcatc ctggcccatg ccttcttccc caagactcac cgagaagggg atgtccactt 600
cgactatgat gagacctgga ctatcgggga tgacc agggc acagacctgc tgcagggtggc 660
agcccataaa tttggccacg tgctggggct gcagcacaca acagcagcca aggccctgat 720
gtccgccttc tacaccttgc gctaccactc agtctcagc ccagatgact gcagggcggt 780
tcaacaccta tatggccagc cctggccccc tgtcacctcc aggaccccag ccctggggccc 840
ccaggctggg atagacacca atgagattgc accgctggag ccagacgccc cgccagatgc 900
ctgtgaggcc tcctttgacg cggctctcac catccgaggc gagctctttt tcttcaaagc 960
gggctttgtg tggcgctcc gtgggggcca gctgcagccc ggctaccag cattggcctc 1020
tcgccactgg cagggactgc ccagccctgt ggacgctgcc ttcgaggatg ccca gggcca 1080
catttggttc ttcaaagggt ctcagtactg ggtgtacgac ggtgaaaagc cagtccctggg 1140
```

223/292

```

ccccgcaccc ctcaccgagc tgggcctggt gaggttcccg gtccatgctg ccttggtctg 1200
gggtcccag aagaacaaga tctacttctt ccgaggcagg gactactggc gtttccaccc 1260
cagcaccg cgtgtagaca gtcccgctgc cccgagggcc actgactgga gaggggtgcc 1320
ctctgagatc gacgctgcct tccaggatgc tgatggctat gcctacttcc tgcgcggccg 1380
cctctactgg aagtttgacc ctgtgaaggt gaaggctctg gaaggcttcc cccgtctcgt 1440
gggtcctgac ttctttggct gtgccgagcc tgccaacact ttctctgac catggcttgg 1500
atgccctcag gggtgctgac ccctgccagg ccacgaatat caggctagag acccatggcc 1560
atctttgtgg ctgtgggcac caggcatggg actgagccca tgtctcctgc agggggatgg 1620
ggtggggtac aaccacatg acaactgccg ggagggccac gcaggctcgtg gtcacctgcc 1680
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tgagcaactg ggctgtaggg caggggccact tcctgaggtc aggtcttggg aggtgcctgc 1980
atctgtctgc cttctggctg acaatcctgg aaatctgttc tccagaatcc agggcaaaaa 2040
gttcacagtc aaatggggag ggggtattctt catgcaggag accccaggcc ctggaggctg 2100
caacatacct caatcctgtc ccaggccgga tcctcctgaa gcccttttcg cagcac tgct 2160
atcctccaaa gccattgtaa atgtgtgtac agtgtgtata aaccttcttc ttcttttttt 2220
tttttaaact gaggattgtc attaaacaca gttgttttct 2260

```

<210> 347

<211> 273

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(273)

<223> 3' terminal sequence. hypothetical protein
mgc13071 (MGC13071) gene.

<400> 347

```

atgtttattg aacgtaacag tatatttcat gtagtttccc ataatttttt catgtactaa 60
ctcatgtaat tctttgtttt ttagagatct gaagtgat tt tacctttact tccttcaett 120
taagccaatc atgaaatttc agtgatttct ggggtgaggg cgaaagggtg tgttacgaat 180
catcggggct gtggccagnt tgctcacgg aggtgcagg aggtggggc ctcactaggg 240
canctggagg agcacggact gcctgccgg cag 273

```

<210> 348

<211> 330

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(330)

<223> 5' terminal sequence. hypothetical protein
mgc13071 (MGC13071) gene.

<400> 348

```

ggagtacaga acattgtggt aggggaaggg actcactttc tcatcccatg tgtacaaaaa 60
ccaattatct ttgactgctg ttctcaacca cgtagtcgnc cagtcacac tggtagcaaa 120
gatttacaga atgtcaacat cacactgtgc atcctcttcc ggcccatcac tagccagctt 180

```


224/292

```
cctcgcatct tcaccagcat tggagaggac tacgatgagt gtgtgctgcc gttcattacc 240
acggagatcc tcaagtcact ggtggctcgc tttgatgctg gagaactaat caccagagg 300
gagcttggtt tccagcngg tgaagnacca 330
```

<210> 349
 <211> 1168
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:prime r

<220>
 <221> misc_feature
 <222> (1)..(1168)
 <223> hypothetical protein mgc13071 (MGC13071)
 gene.

```
<400> 349
aatgatgat agtagtacct acagtatagt gctgtagaa ttacatgagt tagatgtgga 60
ggtcagagtg gaagcaggtg tgagagggtc ccgcagaaga aaacatggct gccaaagtgt 120
ttgagtccat cggcaagttt ggcttgccct tagctgttgc aggaggcatg gtgacctctg 180
ccttatgtaa tgtggatgct gggcacagag ctgccatctt tgaccaattc cgtggagtac 240
agaacattgt ggtaggggaa gggactcact ttctcatccc atgtgtacaa aaaccaatta 300
tctttgactg ctgttctcaa ccacgtagtg cgccagtcac c actggtagc aaagatttac 360
agaatgtcaa catcacactg tgcacacctt tccggcccat cactagccag cttcctcgca 420
tcttcaccag cattggagag gactacgatg agtgtgtgct gccgttcatt accacggaga 480
tcctcaagtc actggtggct cgctttgatg ctggagaact aatcacccag agggagctgg 540
tctccagcca ggtgagcaac aaccttatgg agtgagcagc cacctttggg ctcatctctg 600
acgacgtgtc ttgacacat ctgaccttct tgaaggagtt aacagacagg tggcccccca 660
ggaagcagag agcgccagat ttgtggtgga aaaggcggcc atcatctctg ctgagggtga 720
ctccaaggca gctgagctga tcgccaactc actggccact gcaggggacg gccagagcga 780
gctgtgcaag ctggaagctg cagaagacat tgcataccag ctctcatgct ctcggaacat 840
cacctgcctg ccggcagggc agtccgtgct cctccagctg ccctagttag gccccagcct 900
acctgcacct ccgtgaggca actgggccac agccccgatg attcgtaaca ccacctttcg 960
ccctaccccc agaaatcact gaaatttcat gattggctta aagtgaagga agtaaaggta 1020
aaatcacttc agatctctaa aaaacaaaga attacatgag ttagtacatg aaaaaattat 1080
gggaaactac atgaaatata ctgttacggt caataaacat tagcttctgt atataaaaaa 1140
aaaaaaaaa aaaaaaaaaa aaaaaaaa 1168
```

<210> 350
 <211> 315
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(315)
 <223> 5' terminal sequence. interleukin enhancer
 binding factor 2, 45kd (ILF2) gene.

```
<400> 350
ctggctttga aatcagttct ncgtgatgct acagtgaaga ttctcattac aacagtgcc 60
cccaatcttc gaaaactgga tccagaactc catttgata tcaaagtatt gcagagtgcc 120
ttagcagcca tccgacatgc ccgctgggtc gaggaataat cttctcagtc cacagttaaa 180
gttcnccanc agantactga aggacttgag gattcgtttt ccnggctttg agc cctcaca 240
```

225/292

cccnggatnc ttgaactact aggnccattat gctgtgatga acaacccac caganagcct 300
ttggcnctaa acgtt 315

<210> 351
<211> 1552
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1552)
<223> interleukin enhancer binding factor 2, 45kd
(ILF2) gene.

<400> 351
cggttggtgc ggctccatt gtctgtgtt taaggcgcca tgaggggtga cagaggccgt 60
ggtcgtggtg ggcgctttgg ttccagagga ggcccaggag gag ggttcag gccctttgta 120
ccacatatcc catttgactt ctatttgtgt gaaatggcct tccccgggt caagccagca 180
cctgatgaaa cttccttcag tgaggccttg ctgaagagga atcaggacct ggctcccaat 240
tctgctgaac aggcattctat ctttctctg gtgacaaaaa taaacaatgt gattgataat 300
ctgattgtgg ctccagggac atttgaagt caaattgaag aagttcgaca ggtgggatcc 360
tataaaaagg ggacaatgac tacaggacac aatgtggctg acctggtggt gataactcaag 420
attctgccaa cgttggaagc tgttgctgcc ctggggaaca aagtcgtgga aagcctaaga 480
gcacaggatc cttctgaagt tttaaccatg ctgaccaacg aaactggctt tgaaatcagt 540
tcttctgatg ctacagtga gattctcatt acaacagtgc caccatctt tcgaaaactg 600
gatccagaac tcattttgga tatcaaagta ttgcagagtg ccttagcagc catccgacat 660
gcccgtggtg tcgaggaaaa tgcttctcag tccacagtta aagtctcat cagactactg 720
aaggacttga ggattcgttt tcttggtctt gagccctca c acctggat ccttgacct 780
ctaggccatt atgctgtgat gaacaacccc accagacagc ctttgccct aaacgttgca 840
tacaggcgct gcttgcatg tctggctgca ggactgttc tgccagggtc agtgggtatc 900
actgacctt gtgagagtgg caactttaga gtacacacag tcatgacct agaacagcag 960
gacatggtct gctatacagc tcagactctc gtccgaatcc tctcatggt tggctttagg 1020
aagatccttg gccaggagg tgatgccagc tatcttgctt ctgaaatct tacctgggat 1080
ggagtgatag taacaccttc agaaaaggct tatgagaagc caccagagaa gaaggaagga 1140
gaggaagaag aggagaatac agaaagaacc acctcaagga gaggaagaag aaagcatgg a 1200
aactcaggag tgacattccc ttcactcctt ttcctaccca agggaaagac tggagcctaa 1260
gctgcctgct actggcttta catggtgaca gacattcgt ggataggaa atagcaggag 1320
aaagtaactc catagagtgt cattccactg gttgatattg gcttagctgc cagtctccca 1380
tttgtgacct atgccatcca tctataatgg agg ataccaa catttcttcc taatattcta 1440
taatctccaa ctctgaaaaa cccctctctc aactaatact ttgctgttga aatgttgtga 1500
aatgttaagt gtctggaaat tttttttct aagaaaaact attaaagtac tt 1552

<210> 352
<211> 396
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(396)
<223> 3' terminal sequence. hypothetical protein
flj11307 (FLJ11307) gene.

226/292

<400> 352

ctccattaca ggggttttgc cacttgcgtg gaggataggg ccctgagttc ttacctctaa 60
ggtactggag gtttcagttg tagaatttcc agtattattg cttgagtttg aagacactgt 120
ttcattttta ctttcattat ctgatttttc atcggaactc atacattcaa tatctgcac 180
aaagcctgtt ggatatccca ttgcctgcaa taccttcacc gctacgtgaa agttttgctg 240
ttttcttgga tggctcctgag gcttcatatg ttgtgccatc cacatctaca gacattg tga 300
agactggggg catgaacggg ggccagactg aagataagaa gctatactga agcacaggcc 360
tgatctgaat taagcntcat tagtggcatt ccataa 396

<210> 353

<211> 1858

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> misc_feature

<222> (1)..(1858)

<223> hypothetical protein flj11307 (FLJ11307)
gene.

<400> 353

tcgatgaaag atcctccgga cttattggac aggagaaat gccgaacgc cttggcgtct 60
cttcgacatg ccaaattggt tcaggcaagg gcaaatggat taaaatcatg tgtaat tgtc 120
ctccgcattc tgcgtgattt gtgcaacaga gtccccacat gggcaccatt gaaaggatgg 180
ccactagaac ttatatgtga aaagtctata ggtacttgta atagacctt gggcgctggg 240
gaggccttga gacgagtaat ggagtgttg gcatctggaa tactacttcc tgggggtcct 300
ggtcttcatg atccttgtga gcgagaccca acag atgctc tgagctatat gaccatccag 360
caaaaagaag atattaccca cagtgcacag catgcaactc gactatcagc ctttggccag 420
atttacaaag tgctggagat ggacccctt ccatctagta agccttttca gaagtattcc 480
tggtcagtta ctgataaaga aggtgctggg tcttcagctc taaagaggcc atttgaagat 540
ggattagggg atgataaaga cccaacaag aagatgaaac gaaacttaag gaaaattctg 600
gatagtaaag caatagacct tatgaatgca ctaatgaggc taaatcagat caggcctggg 660
cttcagtata agctcctatc tcagtctggc ccggttcatg cccagctctt cacaatgtct 720
gtagatgtgg atggcacaac atatgaagcc tcaggaccat ccaagaaaac agca aaactt 780
cacgtagcgg tgaaggattt gcaggcaatg ggatatccaa caggctttga tgcagatatt 840
gaatgtatga gttccgatga aaaatcagat aatgaaagta aaaatgaaac agtgtcttca 900
aactcaagca ataatactgg aaattctaca actgaaacct ccagtacctt agaggtaaga 960
actcagggcc ctatcctcac agcaagtggc aa aaaccctg taatggagct caatgaaaaa 1020
agaagaggtc tcaagtatga actcatctca gagactgggt gaagccatga caagcgcttt 1080
gtaatggagg tagaagtaga tggacagaaa ttcagaggcg cagggtccaa taagaaagt 1140
gcaaaggcga gtgcagcttt agctgccttg gagaaactgt tttctggacc caatgcggca 1200
aataataaga aaaagaagat tatccctcag gcaaagggcg ttgtgaatac agctgtgtct 1260
gcagcagtc aagctgttcg gggcagagga agaggaactc taacaagggg agcttttgtt 1320
ggggcgacag ctgctcctgg ctacatagct ccaggctatg gaacaccata tggttacagc 1380
acagctgccc ctgcctatgg tttaccgaag aagatgggtc tggtac ccgt tatgaaattt 1440
ccaacatatc ctgttcccca ctactcattc ttttagcaaa tgacagaagc taattcctat 1500
tgaacaacaa tacagtacaa cacagaatgt tagagaaaaa gcctttttat cctgctttct 1560
ttgaacacat acttgatcaa aattatttgt aaagaacatc tttcctactt tttgatttta 1620
acaaatgcaa attttagttc ctaaaacttg aaaaaaaaaa aagaaaccag ttctgtgaaa 1680
acggtacctc atttctggaa aataacttat accagccctt ctgttctagg gaaataaaa 1740
tctagcagtt caaagtttaa gttttaagag acgtatcaga ttatgtaaaa ttaaatttgt 1800
gaaggatgta tagagtctca aacactgac acaataaac tgctttgttg taacacag 1858

<210> 354

<211> 242

<212> DNA

227/292

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(242)

<223> 5' terminal sequence. v-myb avian

myeloblastosis viral oncogene homolog (MYB) gen e.

<400> 354

```
agaaccccag ctatcaaaag gtcaatctta gaaagctctc caagaactcc tacaccattc 60
aaacatgcac ttgcagctca agaaattaaa tacggtcccc tgaagatgct acctcagaca 120
ccctctcatc tagtagaaga tctgcaggat gtgatcaaac aggaatctga tgaatctgga 180
attgttgctg agtttcaacg aaaatggacc acccttactg aacgaaaatc ntacaacgag 240
gt                                         242
```

<210> 355

<211> 3225

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3225)

<223> v-myb avian myeloblastosis viral oncogene
homolog (MYB) gene.

<400> 355

```
ggcgggcagcg ccctgccgac gccggggagg gacgcaggca ggcggcgggc agcggggaggc 60
ggcaccocgg tgctccccgc ggctctcggc ggagccccgc cgcgcgcgcg gccatggccc 120
gaagaccocg gcacagcata tatagcagtg acgaggatga tgaggacttt gagatgtgtg 180
acctgacta tgatgggctg cttcccaagt ctggaaagcg tcacttgggg aaaacaagg 240
ggaccocgga agaggatgaa aaactgaaga agctggtgga acagaatgga acagatgact 300
ggaaagtatt tgccaattat ctccgaatc gaacagatgt gcagtgccag caccgat ggc 360
agaaagtact aaaccctgag ctcatcaagg gtccttgga caaagaagaa gatcagagag 420
tgatagagct tgtacagaaa tacggtccga aacgttggc tgttattgcc aagcacttaa 480
aggggagaa tggaaaacaa ttagggaga ggtggcataa ccacttgaat ccagaagtta 540
agaaaacctc ctggacagaa gaggaagaca gaatt attta ccaggcacac aagagactgg 600
ggaacagatg ggcagaaatc gcaaagctac tgcctggacg aactgataat gctatcaaga 660
accactggaa ttctacaatg cgtcgaagg tcgaacagga aggttatctg caggagtctt 720
caaaagccag ccagccagca gtggccacaa gcttcagaa gaacagtcac ttgatgggtt 780
ttgctcaggc tccgcctaca gctcaactcc ctgccactgg ccagcccact gtaacaacg 840
actattccta ttaccacatt tctgaagcac aaaatgtctc cagtcatgtt ccataccctg 900
tagcgttaca tgtaaatata gtcaatgtcc ctccagcagc tgccgcagcc attcagagac 960
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tgtcaaccga gaatgagcta aaaggacagc aggtgctacc aacacagAAC cacacatgca 1080
gctaccocgg gtggcacagc accaccattg ccgaccacac cagacctcat ggagacagtg 1140
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ccctacctga agaaagcgcc tcgccagcaa ggtgcatgat cgtccaccag ggcaccattc 1260
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ctcaaaagga aaatactgtt tttagaacc cagctatcaa aaggtcaatc ttagaaagct 1500
ctccaagaac tcctacacca ttcaaactg cacttgacg tcaagaaatt aaatacggtc 1560
ccctgaagat gctacctcag acaccctctc atctagtaga agatctgcag gatgtgatca 1620
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228/292

```

aacaggaatc tgatgaatct ggatttggtg ctgagtttca aga aaatgga ccacccttac 1680
tgaagaaaat caaacaagag gtggaatctc caactgataa atcaggaaac ttcttctgct 1740
cacaccactg ggaaggggac agtctgaata cccaactgtt cacgcagacc tcgcctgtgc 1800
gagatgcacc gaatatctct acaagctccg ttttaatggc accagcatca gaagatgaag 1860
acaatgttct caaagcat tt acagtaccta aaaacaggtc cctggcgagc cccttgacgc 1920
cttgtagcag tacctgggaa cctgcacccg gtggaagat ggaggagcag atgacatctt 1980
ccagtcgaagc tcgtaaatatc gtgaatgcac tctcagcccg gacgctgggc atgtgagaca 2040
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tcaacatgaa acttttcatg aatgggagaa gaacctatct ttgttggtgtg acaacagttg 2160
agagcacgac caagtgcatt tagttgaatg aagtcttctt ggatttcacc caactaaaag 2220
gattttttaa aataaataac agtcttacct aaattattag gtaatgaatt gtagccagtt 2280
gttaatatct taatgcagat ttttttaaaa aaaaacataa aatgatttat ctggtatttt 2340
aaaggatcca acagatcagt attttttctt gtgatgggtt ttttgaaatt tgacacatta 2400
aaaggtactc cagtatttca cttttctcga tcactaaaca tatgcatata tttttaaaaa 2460
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aaatgctcat ttatggtaa tgacattgaa ggtacattta ttgtaccaaa ccattttatg 2580
agttttctgt tagcttgctt taaaaattat tactgtaaga aatagtttta taaaaatta 2640
tatttttatt cagtaattta attttgtaa tgccaaatga aaaacgtttt ttgctgctat 2700
ggctcttagc tgtagacatg ctgctagtat cagaggggca gtaga gcttg gacagaaaga 2760
aaagaaactt ggtgtaggt aattgactat gcaotagtat ttcagacttt ttaattttat 2820
atatatatac atttttttct cttctgcaat acatttgaaa acttgtttg gagactctgc 2880
attttttatt gtgggttttt ttgtattggt ggtttatata agcatgctgt gcacttcttt 2940
tttgggagat gtgtgtgtt catgttctat gttttgttt gtgtgtagcc tgactgtttt 3000
ataatttggg agttctcgat ttgatccgca tcccctgtgg tttctaagt tatggtctca 3060
gaactgttgc atggatcctg tgttgcaac tggggagaca gaaactgtg ttgatagcca 3120
gtcactgcct taagaacatt tgatgcaaga tggccagcac tgaactttt agatatgac g 3180
gtgtacttac tgccttgtag caaaataaag atgtgccctt atttt 3225

```

<210> 356

<211> 369

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(369)

<223> 3' terminal sequence, zinc finger protein 9
(a cellular retroviral nucleic acid binding
protein) (ZNF9) gene.

<400> 356

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gtagttaa at gcagaaagtc ggttttttcc cacccttttc ctctttttac acggcaagta 60
aagctcactg gcttgggagt tgcctctatc tgccaacctt tggccagtga agaggattca 1 20
gagaaaataa tacaaccatc aatcagaaaa aggaggggag acaaaggaaa ataattaggc 180
tgtagctcaa ttgtgcatcc ccgtgcaagg tgccctgact cgccacagcg gtaacagttg 240
acttcacttg tcttgctgca gttgatggct acatgaccag tttcaccaca cctatagcac 300
ttcacttttg tgcagtcttt tttgaatgtg tcccgaattc tcccacaaga atancctttc 360
tgctcanct 369

```

<210> 357

<211> 1500

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1500)
<223> zinc finger protein 9 (a cellular retroviral
nucleic acid binding protein) (ZNF9) gene.

<400> 357
gaattccaaa cagcctctac cttgcgagcc gtcttcccca ggcctgcgtc cgagtctccg 60
ccgctgcggg cccgctccga cgcggaagat ctgactgcag ccatgagcag caatgagtgc 120
ttcaagtgtg gacgatctgg ccactgggcc cgggaatgtc ctactggtgg aggccgtggg 180
cgtggaatga gaagccgtgg cagagggtgt tttacctcgg atagagggtt ccagtttggt 240
tcctcgtctc ttccagatat ttgttatcgc tgtggtgagt ctggtcattc tgccaaggat 300
tgtgatcttc aggaggatgc ctgctataac tgcggtagag gtg gccacat tgccaaggac 360
tgcaaggagc ccaagagaga gcgagagcaa tgctgctaca actgtggcaa accaggccat 420
ctggctcgtg actgcgacca tgcagatgag cagaaatgct attcttgtgg agaattcgga 480
cacattcaaa aagactgcac caaagtgaag tgctataggt gtggtgaaac tggatcatgt 540
gccatcaact gcagcaagac a agtgaagtc aactgttacc gctgtggcga gtcaggggcac 600
cttgcaaggg aatgcacaat tgaggctaca gcctaattat tttcctttgt cgccctcct 660
ttttctgatt gatgtttgta ttattttctc tgaatcctct tcactggcca aaggttgga 720
gatagaggca actcccaggc cagtgcgctt tacttgccgt gtaaaaggag gaaaggggtg 780
gaaaaaaacc gactttctgc atttaactac aaaaaaagt tatgtttagt ttggtagagg 840
tgttatgtat aatgctttgt taaagaaccc ctttccgtg ccactggtga atagggttg 900
atgaatggga agagttgagt cagaccagta agcccgctc gggttccttg aacatgttcc 960
catgtaggag gtaaaaccaa ttctggaagt gtctatgaac t tccataaat aactttaatt 1020
ttagtataat gatggtcttg gattgtctga cctcagtagc tattaataa catcaagtaa 1080
catctgtatc aggccctaca tagaacatac agttgagtgg gagtaacaa aaagataaac 1140
atgcgtgtta atggctgttc gagagaaatc ggaataaaaag cctaaacagg aacaacttca 1200
tcacagtgtt gatgttggac acatagatgg tgatggcaaa ggtttagaac acattatatt 1260
caaagactaa atctaaaacc cagagtaaac atcaatgctc agagttagca taatttgagg 1320
ctattcagga attgcagaga aatgcatttt cacagaaatc aagatgttat tttgtatatac 1380
tatatcactt agacaactgt gtttcatttg ctgtaatcag tttttaaag tcaga tggaa 1440
agagcaactg aagtcctaga aaatagaaat gtaattttaa actattccaa taaagctgga 1500

<210> 358
<211> 425
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(425)
<223> 3' terminal sequence. camp responsive
element modulator (CREM) gene.

<400> 358
ttttttactt ctgcaagatc ttttatatta cacagtagag ttaaaaactg tagtaaattg 60
tcagatatatt aaatgagcac caaacactac aaatgcaac caacatgggt ctattaaaaa 120
ctcnccttga ctatggcatt caaggacagc aatacaat ct tttttttttt taacaaagca 180
actaatataa aaatctgcaa atgccatata ttcataatcta ggctattctt cncatatagg 240
catgtcatta gatagacttt ctttctatcc tttccngagg natttttttg nggtttacnt 300
ttattgnact gctggatgca ttatttttga tcatcctttc ctaaaatgnt ttaaagacct 360
gcaataaatt ttattgcata ggacacnatt ggtgncacat agaatggggag cngcaagtat 420
gtggc 425

<210> 359

230/292

<211> 232
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(232)
 <223> 5' terminal sequence. camp responsive
 element modulator (CREM) gene.

<400> 359
 ggatttagag ttaactagct caccactgcc tctgcctcca agctgccttt tagactgaat 60
 agcttttctt gttagcccta ctttaacatt tcttttgaag tgggtgtctg cttgaagagg 120
 gaaacacgtc atgaaactgt aatgcatgaa cagaactcag gagttgtctg gccagcttag 180
 tgctgccact ggtgacatgc caacttacca gatccgagct cctantgnng ct 232

<210> 360
 <211> 1431
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:prime r

<220>
 <221> misc_feature
 <222> (1)..(1431)
 <223> camp responsive element modulator (CREM)
 gene.

<400> 360
 atgaccatgg aaacagttga atcccagcat gatggaagta taacagcttc tttgacagag 60
 agcaagtctg ctcatgtgca gactcagact gggcaaattt caatccctgc tttagctcag 120
 tgcagtgaag tgagatcagg caccagaaga ggctcccag ctgtaactct agtgacagta 180
 ccttcggggc aaactataca tgtccaggga gtaattcaga caccacagcc atgggttatt 240
 cagtcacatc aaatacacac cgttcaggta gcagcaattg cagagacaga tgaatctgca 300
 gaatcagaag gtgtgaattga ttctcataaa cgtagagaaa t cctttcacg aagaccctct 360
 tataggaaaa tactgaatga actgtcctct gatgtgcctg gtgttcccaa gattgaagaa 420
 gagagatcag aggaagaagg aacaccacct agtattgcta ccatggcagt accaactagc 480
 atatatcaga ctagcacggg gcaatacatt gctatagccc aagggtggaac aatccagatt 540
 tctaaccacg gatctgatgg tggtcaggga ctgcaggcat taacaatgac aaattcagga 600
 gctcctccac caggtgctac aattgtacag tacgcagcac aatcagctga tggcacacag 660
 cagttctttg tcccaggcag ccaggttggt gttcaagctg ccactggtga catgccaaact 720
 taccagatcc gagctcctac tgctgctttg ccacaggag tggatgatgc tgcacgccc 780
 ggaagtttgc acagtcccca gcagctggca gaagaagcaa cagcgaacg agagctgagg 840
 ctaatgaaaa acagagaagc tgcccgggag tgtcgcagga agaagaaaga atatgtcaaa 900
 tgtcttgaaa atcgtgtggc tgtgcttgaa aaccaaaca agactctcat tgaggaaactc 960
 aaggccctca aagatcttta ttgccataaa gttagagtaac tgtctttgac ttggaccttg 1020
 tttactctaa tcaaggcagg agatgcagca gtctactta ttgccatgtg gacttgtggg 1080
 aaggacacgt gtgaccctta agaattccagt ttggattagt gtttgaaatt gaattgggaa 1140
 tgttgttcca ggatgtgga tgacagctga tcacacttac cgagcttact ttgatctggt 1200
 tgtcaatagc atgcataaaa tgctttgttt gccctttgct tctgcttttt ttcagggaag 1260
 ctgccaaaaga atgtcgacgt cgaaagaaag aatatgtaaa atgcctggag agccgagttg 1320
 cagtgctgga agtccagaac aagaagctta tagaggaact tgaaacctg aaagacattt 1380
 gttctcccaa aactgattac tagaaatatt taactatgaa ctgattacag a 1431

231/292

<210> 361
<211> 457
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(457)
<223> 3' terminal sequence. cathepsin b (CTSB)
gene.

<400> 361
caagttggag aaacctttta ttggcacagg cattccttgt taacttgaca gggggaagct 60
gtaatttttc aaaaacagta aaagctgggt tctcctaaac tattttcctt gtggtagtag 120
agatcagtg gtcagaaaca actcctgacc acttggtttc cttttgagcc gcgtcattag 180
gaggcaatct gtaaaactag cacaggtctc ccgctgttc actggctcac ccacatg att 240
agcagagtgc acgaaaaaat aaaacttcta ttaaagaatc atgctgagca caacatcaga 300
gaggttgtga cattgcaaac tcgatagatg cagggggcct gggagactgg cgttctccaa 360
agggctccca acaccatctc tctctgatt tctgtgacaa atgtggaagc tacttgcttg 420
gagggtactg gggaactgat gggggaactt tcatc cg 457

<210> 362
<211> 401
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(401)
<223> 3' terminal sequence. melan -a (MLANA) gene.

<400> 362
atcatgcatt gcaacattta ttgatggagt tttcccaatt taatatttct catcatttcc 60
tcacatgatt agtactgcta gcgacctac taaaatttta aactgactt attattagag 120
atggcttgca tttttcctac accattccaa aggagaacat tagatgtctg tattaaattc 180
aagcaaaagt gtgagagaaa taatttcagc atgtctcagg tgtctcgt g gcncttaagg 240
tgaataaggt ggtggtgact gttctgcaga gagtttctca taagcaggtg gagcattggg 300
aaccacaggt tcacagtgtt tctcttgaag agacactttg ctgtcccgat gatcaaacc 360
ttcttgtggg catcttcctg ttaaggcaca ttgaggccaa c 401

<210> 363
<211> 370
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(370)
<223> 5' terminal sequence. melan -a (MLANA) gene.

232/292

<400> 363

attaaggaag gtgtcctgtg ccctgaccct acaagatgcc aagagaagat gctcacttca 6 0
tctatggtta cccaagaag gggcacggcc actcttacac cacggctgaa gaggccgctg 120
ggatcggcat cctgacagtg atcctgggag tcttactgct catcggctgt tggatttgta 180
gaagacgaaa tggatacaga gccttgatgg ataaaagtct tcatgttggc actcaatgtg 240
cttaacaaga agatgcccac aagaagggtt tgatcatcgg gacagcaaag tgtctcttca 300
agagaaaaac tgtgaacctg tggttcccaa tgctccacct gcttatggag aaactctctg 360
cagaacagtc 370

<210> 364

<211> 1524

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1524)

<223> melan-a (MLANA) gene.

<400> 364

agcagacaga ggactctcat taaggaaggt gtctgtgcc ctgaccctac aagatgcca 60
gagaagatgc tcacttcac tatggttacc ccaagaagg gcacggccac tcttacacca 120
cggctgaaga ggccgctggg atcggcatcc tgacagtgat cctgggagtc ttactgctca 180
tcggctgttg gtattgtaga agacgaaatg gatacagagc cttgatggat aaaagtcttc 240
atgttggcac tcaatgtgcc ttaacaagaa gatgccaca agaagggtt gatcatcggg 300
acagcaaagt gtctcttcaa gagaaaaact gtgaacctgt gggtccc aat gctccacctg 360
cttatgagaa actctctgca gaacagtcac caccacctta ttcacctta gagccagcga 420
gacacctgag acatgctgaa attatttctc tcacactttt gcttgaattt aatacagaca 480
tctaattgtc tcctttggaa tgggttagga aaaatgcaag ccactctctaa taataagtca 540
gtgttaaaat tttagtaggt ccgct agcag tactaatcat gtgaggaaat gatgagaaat 600
attaaattgg gaaaactoca tcaataaatg ttgcaatgca tgatactatc tgtgccagag 660
gtaatgttag taaatccatg gtgttatttt ctgagagaca gaattcaagt gggattctcg 720
gggccatcca atttctcttt acttgaaatt tggctaataa caaactagtc aggttttctga 780
accttgaccg acatgaactg tacacagaat tgttcagta ctatggagt ctcacaaagg 840
atacttttac aggttaagac aaagggttga ctggcctatt tatctgatca agaacatgtc 900
agcaatgtct ctttgtgctc taaaattcta ttatactaca ataatatatt gtaaagatcc 960
tatagctctt tttttttgag atggagtttc gcttttgtg ccag gctgg agtgcaatgg 1020
cgcgatcttg gctcaccata acctccgctt ccagggttca agcaattctc ctgccttagc 1080
ctcctgagta gctgggatta caggcgtgag ccactatgcc tgactaattt tgtagtttta 1140
gtagagacgg ggtttctcca tgttggtcag gctgggtctca aactcctgac ctcaggtgat 1200
ctgcccgcct cagcctccca aagtgctgga attacaggcg tgagccacca cgctgggctg 1260
gatcctatat cttaggtaag acatataacg cagtctaatt acatttcact tcaaggctca 1320
atgctattct aactaatgac aagtattttc tactaaacca gaaattggta gaaggattta 1380
aataagtaaa agctactatg tactgcctta gtgctgatgc ctgtgtactg ccttaaatg t 1440
acctatggca atttagctct cttgggttcc caaatccctc tcacaagaat gtgcagaaga 1500
aatcataaag gatcagagat tctg 1524

<210> 365

<211> 556

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:p rimer

<220>

233/292

<221> misc_feature
<222> (1)..(556)
<223> 3' terminal sequence. apr -1 protein (APR-1)
gene.

<400> 365
actattcggtt aggccttttat ttttctctat gttctgcagt aactaaggaa aatcatggta 60
aatgtcaatc ttcacacaac agcagacaca aagggtttca gaaacgtcag atatgaag aa 120
atcctccatc cttcttcaac attttactgg gtatttcaac ttcaaaagaa cagcttattt 180
ctataagtgc tgtacaagat catagattat gatggaacga cttcatttta gaacgttagc 240
aaaactgtta tactaaatgt caatgacagg aaacaaagaa aaaaatttgt tcaattatat 300
ttttaaacat attgttattc tcaacaaacg gaattt taaa acgaatacaa ttttccatta 360
tcaaaaagca aacactctat ttgcgagttg aacaatgac actgacacaa aatatacnaat 420
acagtgtccc ccgcccccaa tcgacatcat tttccactta gggaccctgg catccactcc 480
ctgggggtac ccgtgactcc ncctttacac cccccagggg ctggcctcag atctacctaa 540
gggnggggat aacc cc 556

<210> 366
<211> 464
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(464)
<223> 5' terminal sequence. apr -1 protein (APR-1)
gene.

<400> 366
aacagcgcca aggaagctct ggtctggaaa gtgctgggga agttaggaat gcagcctgga 60
cgtcagcaca gcattctttg agatccgaag aagatcgta cagaagagtt tgtgcgcaga 120
gggtacctga tttataaacc ggtgccccgt agcagtcagg tggagtatga gttcttctgg 180
gggccccgag cacacg tgga atcgagcaaa ctgaaagtca tgcattttgt ggcaagggtt 240
cgtaaccgat gctctaaaga ctggccttgt aattatgact gggattcgga cgatgatgca 300
gagggttagg ctatcctcaa ttcagggtgt aggggttatt ccgcccccta agtagatctg 360
gaggcagacc cttgggggtt gtaaaagaga gtnacaggt cccccaaagg agtagatg nc 420
aaggggacct aagttgcaaa atgatgtcga ttttggggcc gggg 464

<210> 367
<211> 1476
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1476)
<223> apr-1 protein (APR-1) gene.

<400> 367
ctggaagaat tcgcgtggca ggagaggcgg ggccaatttt gctgagcttt ctgcggggct 60
tgcagctgcg gcaagtgcgt gcggcggtcg ctgcgcgaag tcagctggcg tgggaactac 120
cctttgtagc tgagaacggc ttgtttattg ctacaaagac tctattgaca ttggtagctt 180
cagcggcagc agcttct tac ggtataaagc tgttgcttcc tgaagaggct acaagcatcc 240

234/292

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ttccctagga ctgctgtaag ctttgagcct ctagcaggag acatgcctcg gggacgaaag 300
agtcggcgcc gcogtaatgc gagagccgca gaagagaacc gcaacaatcg caaaatccag 360
gcctcagagg cctccgagac ccctatggcc gcctctgtgg tagcgagcac ccccgaaga c 420
gacctgagcg gccccgagga agacccgagc actccagagg aggcctctac caccctgaa 480
gaagcctcga gcaactgccc agcacaaaag ccttcagtgc cccggagcaa ttttcagggc 540
accaagaaaa gtctcctgat gtctatatta gcgctcatct tcatcatggg caacagcgcc 600
aaggaagctc tggctctggaa agtgctgggg aagtttag gaa tgcagcctgg acgtcagcac 660
agcatctttg gagatccgaa gaagatcgtc acagaagagt ttgtgcgcag aggttacctg 720
atttataaac cgggtgcccc tagcagtcgc gtggagtatg agttcttctg ggggccccga 780
gcacacgtgg aatcgagcaa actgaaagtc atgcattttg tggcaagggt tcgtaaccga 840
tgctctaaag actgg ccttg taattatgac tgggattcgg acgatgatgc agaggttgag 900
gctatcctca attcaggtgc taggggttat tccgccccct aagtagatct gaggcagacc 960
cttgggggtg taaaagagag tcacaggtac cccaaggagt agatgccagg gtctaagtt 1020
gaaaatgatg tcgattgggg gcgggggaca ctgtatttga tatttgatgat cagtga tcat 1080
tgttcaactg cgaaatagag tgtttgcttt tgataatgga aaattgtatt cgttttaaaa 1140
ttccgtttgt tgagaataac aatatgttta aaaatataat tgaacaaatt tttttctttg 1200
tttctgttca ttgacattta gtataacagt tttgctaacg ttctaaaatg aagtcgttcc 1260
atcataatct atgatcttgt acagcactta tagaataaag ctgttctttt gaagttgaaa 1320
taccagtaa aatgttgaag aaggatggag gatttcttca tatctgacgt ttctgaaacc 1380
ctttgtgtct gctgttgtgt gaagattgac atttaccatg attttcctta gttacttgac 1440
gtcttgatc tctttttatt ttoggattgc ttatca 1476

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<210> 368

<211> 436

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(436)

<223> 3' terminal sequence. ets variant gene 5
(ets-related molecule) (ETV5) gene.

<400> 368

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cgtttttttg 'cttttaaatca caaaactaca aaaatcagtt tataaactgt ttttcaaaa 60
caaccaccaa aacaaaacaa tcccccaaat cagggcaaaa caaaatactg tcaaaagtgt 120
taatcgccct tctcctaaaa taaaagtcac ccacactcag ccacgtgatt gggaagagaa 180
agggggcttg ctctacttgg cgaccacatg gccgggtggt tcccaa gagt agccatgggt 240
tatgattttg agaaccacgg agngcgaaac agctgttctg actgcccccc tttttctaga 300
caaggggtaa tatttcagat tcagctagaa gagctttcca atgtttaaga tgtattttta 360
acccttaatg gtttgagcct cccaactta gcctacttac ttttcnaagg gtttgtgatt 420
tttcaacaaa ttgtgc 436

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<210> 369

<211> 414

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(414)

<223> 5' terminal sequence. ets variant gene 5
(ets-related molecule) (ETV5) gene.

235/292

<400> 369
ggttgctcgg cgctggggca tccagaagaa ccggccagcc atgaactatg acaagctgag 60
ccgctctctc cgctattact atgaaaaggg catcatgcag aagggtggctg gagagcgata 120
cgtctacaaa tttgtctgtg acccagatgc cctcttctcc atggctttcc cggataacca 180
gcgtccgttc ctgaaggcag agtccgagtg ccacctcagc gaggaggaca cctgcccgt 240
gacccacttt gaagacagcc ccgcttacct cctggacatg gaccgctgca gcagcctccc 300
ctatgccgaa ggtttgttta ctaagtttct gagtggcgga gtgnccaaac cctaggagct 360
agcagttccc attcagggca aacaagnggc agtgngnttt gtt ttgtgtt tttt 414

<210> 370

<211> 249

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(249)

<223> 5' terminal sequence. cd69 antigen (p60,
early t-cell activation antigen) (CD69) gene.

<400> 370
ataataagga aacgtgttca cttattgact attatagaat ggaactcatg gaaatctgtg 60
tcagtggatg ctgctctgtg gtccgaagtc ttccatagag actttgtgaa aaaaaatttt 120
atagtgtctt gggaattttc ttccaaacag aactatggaa aaaaaggaag aaattccagg 180
aaaatctgca ctgtgggctt ttattgccat gagctagaag catcacaggg tgaccaataa 240
cccngacgc 249

<210> 371

<211> 1702

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1702)

<223> cd69 antigen (p60, early t-cell activation
antigen) (CD69) gene.

<400> 371
agactcaaca agagctccag caaagacttt cactgtagct tgacttgacc tgagattaac 60
tagggaatct tgagaataaa gatgagctct gaaaattgtt tcgtagcaga gaacagct ct 120
ttgcatccgg agagtggaca agaaaatgat gccaccagtc cccatttctc aacacgtcat 180
gaagggtcct tccaagttcc tgtcctgtgt gctgtaatga atgtgggtctt catcaccatt 240
ttaatcatag ctctcattgc cttatcagtg ggccaataca attgtccagg ccaatacaca 300
ttctcaatgc catcagacag ccattgttct tcatgc tctg aggactgggt tggctaccag 360
aggaaatgct actttatttc tactgtgaag aggagctgga cttcagccca aaatgcttgt 420
tctgaacatg gtgctactct tgtgtcatt gattctgaaa aggacatgaa ctttctaaaa 480
cgatacgag gtagagagga aactgggtt ggactgaaaa aggaacctgg tcacccatgg 540
aagtgggtcaa atggcaaaga atttaacaac tggttcaacg ttacaggggc tgacaagtgt 600
gtttttctga aaaacacaga ggtcagcagc atggaatgtg agaagaattt atactggata 660
tgtaacaaac cttacaaata ataaggaaac atgttcactt attgactatt atagaatgga 720
actcaaggaa atctgtgtca gtggatgctg ctctgtggtc cgaagtcttc cataga gact 780

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```

ttgtgaaaaa aaattttata gtgtcttggg aattttcttc caaacagaac tatggaaaaa 840
aaggaagaaa ttccaggaaa atctgcactg tgggctttta ttgcatgag ctagaagcat 900
cacagggtga ccaataacca tgcccaagaa tgagaagaat gactatgcaa cctttggatg 960
cactttatat tattttgaat ccagaaataa tgaa ataact aggcgtggac ttactattta 1020
ttgctgaatg actaccaaca gtgagagccc ttcatgcatt tgcactactg gaaggagtta 1080
gatgttggtg ctagatactg aatgtaaaca aaggaattat ggctggtaac atagggtttt 1140
agtctaattg aatcccttaa actcagggag catttataaa tggacaaatg cttatgaaac 1200
taagatttgt aatatttctc tctttttaga gaaatttgcc aatttacttt gttatttttc 1260
cccaaaaaga atgggatgat cgtgtattta ttttttact tcctcagctg tagacaggtc 1320
cttttcgatg gtacatatat ctttgccttt ataactcttt atacagtgtc ttacagagaa 1380
aagacataag caaagactat gaggaatatt tgcaagacat agaatagt gt tggaaaatgt 1440
gcaatatgtg atgtggcaaa tctctattag gaaatattct gtaatcttca gacctagaat 1500
aatactagtc ttataatagg tttgtgactt tcctaaatca attctattac gtgcaatact 1560
tcaatacttc atttaaaata tttttatgtg caataaaatg tatttgtttg tattttgtgt 1620
tcagtacaat tataagctgt tt ttatatat gtgaaataaa agtagaataa acacaaaaaa 1680
aaaaaaaaaa aaaaaaaaaa aa

```

<210> 372

<211> 585

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(585)

<223> 3' terminal sequence. oncogene tc21 (TC21) gene.

<400> 372

```

gtaggcagta tgattccaaa agttaaaaat tatttcacaa cctgtagctt cagcttggca 60
aacagcttag attccaaaaa tgattcatct ctattaaaaa gtaagcactt aaaaaaagag 120
catgtctgtg tatatagaca tat atttttaa aggaatcaga taatctttga agcagcctta 180
gtgtttcctt taaatttgtc tggaaatgac cattgtatta gcttcacaga aaggactagc 240
cagcttcttc gtctaaggct aacatggtga tcatttgtct aaggctagaa aggtaccaac 300
aagatgtaaa ctgaggagag aaagagaaga tgagggcttt tcctggccgt tggtagctaa 360
aactgaaggg attctagaaa atgacacaat gccagccttt cntgtctttt tctttccgtg 420
ttggttcngg tgaaggagga cattcctggc cctggaaatt tccnggataa cccggacaag 480
ttcatgggaa agcttgatct acattcatcc taatccttgc cggatgccnc catgtatgtt 540
acctaagctg ccggcaacgg tngcctctnc cggggtaccg gcc ng

```

<210> 373

<211> 451

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(451)

<223> 5' terminal sequence. oncogene tc21 (TC21) gene.

<400> 373

```

gattcttaca caaagcagtg tgtgatagat gacagagcag cccggctaga tattttggat 60

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acagcaggac aagaagagtt tggagccatg agagaacagt atatgaggac tggcgaaggc 120
ttcctgttgg tcttttcagt cacagataga ggcagttttg aagaaatcta taagtttcaa 180
agacagattc tcagagtaaa ggatcgtgat gatttcccaa tgattt taat tggtaataaaa 240
gcagatctgg atcatcaaag acaggttaaca caggaagaag gacaacagtt agcacggcag 300
cttaaggtaa catacatgga ggcacagca aagattagga tgaatgtaga tcaantttcc 360
atgaacttgt ccgggttatc aggaaatttc aagancagga atgtcctctt cacagaccac 420
acggaaaagaa aagccagaaa gctg cattgt g 451
```

<210> 374

<211> 425

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(425)

<223> 3' terminal sequence. cd44 antigen (homing
function and indian blood group system) (CD44)
gene.

<400> 374

```
gaagatcgaa gaagtacaga tatttattat gaatcagttt aaaccctttt gtgcctctga 60
caaagtaact ttaaaaaatt atactgatca aaggactgat ccagggttta atatttcaa 120
aacacagata aatagtttac tacagataaa tagcttcacc c tttggtgtc ctcccagaag 180
catctgaaaa atttctagag ggggtctgtt gaagatgtgt aactagtaca cccaacccc 240
caacctcagt ggaaagcaat gccagggat taggctatgg aagggcaaaa tggaccatt 300
caaatttctt cccagggacc aggccctatt aaccctggga aatgtcctta gctgggtggg 360
gaaaggttgg cgattcagga atacatatgt gtagtttttg ttagaagcca tccatagcac 420
acccg 425
```

<210> 375

<211> 478

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(478)

<223> 5' terminal sequence. cd44 antigen (homing
function and indian blood group system) (CD44)
gene.

<400> 375

```
ggcgttccag ttcccacttg gaggccttc atccctoggg tgtgctatgg atggcttcta 60
acaaaaacta cacatatgta ttcctgatcg ccaacct ttc cccaccagc taaggacatt 120
tcccagggtt aatagggcct ggtccctggg aggaaatttg aatgggtcca ttttgccctt 180
ccatagccta atccctgggc attgctttcc actgaggttg ggggttggg tgtactagt 240
acacatcttc aacagacccc ctctangaaa ttttccagat gcttctggga gacacccaaa 300
ggggaaagct attta tctgt agtaaactat ttatctgtgt ttttgaaata ttaaaccctg 360
gatcagtcct ttgatcagta taaattttt aaagttactt ttgtcagagg caccaaagg 420
tttaaactga ttcataaata aatatcnnga cttcctcgat cttccaaaaa aaaaaaa 478
```

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<210> 376
<211> 1794
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1794)
<223> cd44 antigen (homing function and indian
blood group system) (CD44) gene.

<400> 376
cccgcgcct ccgttcgctc cggacacccat ggacaagttt tgggtggcacg ca gcctgggg 60
actctgctc gtgcgcgtga gcctggcgca gatcgatttg aatataacct gccgctttgc 120
aggtgtattc cacgtggaga aaaatggtcg ctacagcatc tctoggacgg aggcgcgtga 180
cctctgcaag gctttcaata gcacctgcc cacaatggcc cagatggaga aagctctgag 240
catcggattt gagacctgca ggtatgggtt c atagaaggg catgtggtga ttccccggat 300
ccaccccaac tccatctgtg cagcaaacaa cacaggggtg tacatcctca catacaaac 360
ctcccagtat gacacatatt gcttcaatgc ttcaagctcca cctgaagaag attgtacatc 420
agtcacagac ctgcccattg cctttgatgg accaattacc ataactattg ttaaccgtga 480
tggcaccgcg tatgtccaga aaggagaata cagaacgaat cctgaagaca tctaccccag 540
caaccctact gatgatgacg tgagcagcgg ctctccagt gaaaggagca gcacttcagg 600
aggttacatc ttttacacct tttctactgt acaccccatc ccagacgaag acagtccctg 660
gatcaccgac agcacagaca gaatccctgc taccagagac caagacacat t ccaccccag 720
tgggggggtc cataccactc atggatctga atcagatgga cactcacatg ggagtcaaga 780
aggtggagca aacacaacct ctggtcctat aaggacaccc caaattccag aatggctgat 840
catcttgcca tccctcttgg ccttggtttt gattcttgca gtttgcatg cagtcaacag 900
togaagaagg tgtgggcaga agaaaaagct agtgatcaac agtggcaatg gagctgtgga 960
ggacagaaag ccaagtggac tcaacggaga ggccagcaag tctcaggaaa tgggtgcattt 1020
ggtgaacaag gagtcgtcag aaactccaga ccagtttatg acagctgatg agacaaggaa 1080
cctgcagaat gtggacatga agattgggtg gtaacaccta caccattatc ttggaaagaa 1140
acaaccgttg gaaacataac cattacaggg agctgggaca cttaacagat gcaatgtgct 1200
actgattgtt tcattgcgaa tcttttttag cataaaattt tctactcttt ttgttttttg 1260
tgttttgttc tttaaagtca ggtccaattt gtaaaaacag cattgctttg taaattaggg 1320
cccaattaat aatcagcaag aatttgatcg ttcagttcca ctg gaggcc ttcacctcgt 1380
ggtgtgctat ggatggcttc taacaaaaac tacacatatg tattcctgat cgccaacctt 1440
tcccaccaca gctaaggaca ttcccagggt ttaatagggc ctggtccctg ggaggaaatt 1500
tgaatgggtc cattttgccc ttccatagcc taatccctgg gcattgcttt ccactgaggt 1560
tgggggtgac tagttacac a tottcaacag accccctcta gaaatttttc agatgcttct 1620
gggagacacc aaagggtgaa gctatttatc ttagtagaac tatattatctg tgtttttgaa 1680
atattaaacc ctggatcagt cctttgatca gtataatttt ttaaagttac tttgtcagag 1740
gcacaaaagg gtttaaactg attcataata aatatctgta cttcttcgat ctcc 1794

<210> 377
<211> 452
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(452)
<223> 3' terminal sequence. cyclin dependent
kinase inhibitor 3 (cdk2-associated dual
specificity phosphatase) (CDKN3) gene.

<400> 377
ttttgtcaat aaaactttag gaatatctgc acatgtacat ttacattcaa gttgataaca 60
ctgggtggttt cttttcaata caaattatgc tagagaactg acatttcaga catggtcata 120
tatatgctat ttgaattcct ttatcttcga tacagatctt gattgtgaat ctc ttgatga 180
tagatgtgca gctaatttgt cccgaaactc atgaagataa ttgtattgct tgatggctctg 240
tattgccccg gatcctctta ggtctcgag gctgtctatg gcttgctctg gtgatattgt 300
gtcagacagg tatagtagga gacaagcagc tacaagacaa gatctcccaa gtcctccata 360
gcagtgtatt aagggttttc cggtaat t aaggcaggt tgtaagcnc tccattattt 420
cacagcagct ggccatgton ggagtcctcc ca 452

<210> 378
<211> 472
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(472)
<223> 5' terminal sequence. cyclin-dependent
kinase inhibitor 3 (cdk2-associated dual
specificity phosphatase) (CDKN3) gene.

<400> 378
ggcacgagcg gcaactggtc tcgacgtggg gcgccanga ctgaagccca ngntcaata 60
caaacaagtg agtttgactc atcagatg aa gagcctattg aagatgaaca gactccaatt 120
catatatcat ggctatcttt gtcacgagtg aattgttctc agtttctcgg ttatgtgct 180
cttccaggtt gtaaatttaa agatgttaga agaaatgtcc aaaaagatac agaagaacta 240
aagagctgtg gtatacaacg acataattgt tttctgcacc agaggggaac tgtcaaaaata 300
tagagtccca aaccttcttg atctctacca gcaatgtgga attatcacc atcatcatcc 360
aatccgcaga tggagggact cctgacatag ccagctgctg tgaaataatg gaagagctta 420
caacctgcct taaaaattac cgaaaaacct taatacactg ctatggagga ct 472

<210> 379
<211> 639
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(639)
<223> cyclin-dependent kinase inhibitor 3
(cdk2-associated dual specificity phosphatase)
(CDKN3) gene.

<400> 379
atggagccgc ccagttcaat acaacaagt gagtttgact catcagatga agagcctatt 60
gaagatgaac agactccaat tcatatatca tggctatctt tgtcacgagt gaattgttct 120
cagtttctcg gtttatgtgc tcttccaggt tgtaaat tta aagatgttag aagaaatgtc 180
caaaaagata cagaagaact aaagagctgt ggtatacaag acataattgt tttctgcacc 240
agaggggaac tgtcaaaaata tagagtccca aaccttcttg atctctacca gcaatgtgga 300
attatcacc atcatcatcc aatcgcagat ggagggactc ctgacatagc cagctgctgt 360
gaaataatgg aagagcttac aacctgcctt aaaaattacc gaaaaacctt aatacactgc 420

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tatggaggac ttgggagatc ttgtcttgta gctgcttgt c tctactata cctgtctgac 480
acaatatcac cagagcaagc catagacagc ctgcgagacc taagaggatc cggggcaata 540
cagaccatca agcaatacaa ttatcttcat gagtttcggg acaaattagc tgcacatcta 600
tcatcaagag attcacaatc aagatctgta tcaagataa 639

<210> 380

<211> 487

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(487)

<223> 5' terminal sequence. max -interacting
protein 1 (MXI1) gene.

<400> 380

aagtggcgac tggaacagct gcagggtcct caggagatgg aacgaatacg aatggacaga 60
attggatcaa ctatttcttc agatcgttct gattcagagc gagaggagat tgaagtggat 120
gttgaaagca cagagttctc ccatggagaa gtggacaata taagtaccac cagcatcagt 180
gacattgatg accacagcag cctgccgagt attgggagtg acgagggtac tccagtgccca 240
gtgtcaaaact ttcatctact tcatagaacc cagcatgaca taacagtgcga gggaaaatat 300
tcactggggc attcatacaa acaatctctt aaattgggtt catgatgcag tctcctcttt 360
aaaacaaaac aaaacaaaac aaactatact tgaacaaaag ggtcagagga ctgttttaag 420
caataactag caaaagtggg cagctcccaa gagacaattt cagatttcatt ttggaaatcc 480
catttta 487

<210> 381

<211> 2416

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2416)

<223> max-interacting protein 1 (MXI1) gene.

<400> 381

agattatgat cgcctgaggg ccctctccta cccagatacc gatgttatac tgatgtgttt 60
ttcctttttt tttttttttt ttaagtaat taagggtagt taaattattt aaagtataca 120
aagtccaaac agccaggggt aaggtctcca agaggccttc ccagggttaag ggagtgcgga 180
gaggcccccg tcgccaccgg cgggtgccat ggagcgggtg aagatgatca acgtgcagcg 240
tctgtctggag gctgccgagt ttttgagcgg ccgggagcga gagtgtgaac atggctacgc 300
ctcttcattc ccgtccatgc cgagcccccg actgcagcat tcaaagcccc cacggagggtt 360
gagccgggca cagaacacac gcagcggggc gagcaacacc a gcactgccca acagatctac 420
acacaatgag ctggaaaaga atcgacgagc tcatctgcgc ctttgtttag aacgcttaaa 480
agttctgatt ccactaggac cagactgcac ccggcacaca acacttggtt tgctcaacaa 540
agccaaagca cacatcaaga aacttgaaga agctgaaaga aaaagccagc accagctcga 600
gaatttgga cgaacacaga gatttttaaa gtggcgactg gaacagctgc agggctctca 660
ggagatggaa cgaatacga tggacagcat tggatcaact atttcttcag atcgttctga 720
ttcagagcga gaggagattg aagtggatgt tgaaagcaca gagttctccc atggagaagt 780
ggacaatata agtaccacca gcatcagtga cattgatgac cacagcagcc tgccgagtat 8 40
tgggagtgac gagggttact ccagtgccag tgtcaaactt tcattcactt catagaaccc 900

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agcatgacat aacagtgcag ggcaaaatat tcaactgggcc aattcaatac aaacaatctc 960
ttaaattggg ttcatgatgc agtctcctct ttaaaacaaa acaaaacaaa acaaaactat 1020
acttgaacaa aagggtcaga ggacctgtat ttaagcaaa t acttagcaaa aagtggggca 1080
gagctcccaa ggagaacaaa tattcagaat attcatattg gaaaaatcac aatttttaat 1140
ggcagcagaa aacttgtgtg aaattttctt gatttgagtt gattgagaag aggacattgg 1200
agatgccatc ctctttctct tttctggtt gtcatacta cattgagtag acacatttaa 1260
ggatgggggt atgaaccctt cctgagcttt atggtcctaa aagcaaaata aaaactattc 1320
gaatgaaaag acaagaaaat caggtattaa tcttgatag ctaataatga gctattaaaa 1380
ctcagcctgg gacagtttat catgaagcct gtggatgac aatcctttat tattattttt 1440
tttttttgaa aaaagctcat ttcatgctct gcaaaaggag agactcccat ga agcctttt 1500
gaaagggatc atcatgcagc tcaactttct gttggattcc atgctaagca agctaaccct 1560
atcctgcatt gttagcacta ggcaccagc tgccacctct ccacctgct gcccttaggc 1620
cacatgggag cagtccatgc atgacagcct ctatcctaca aggcctatga gtatggattg 1680
ggggggccaa aaggaaaaag ctccatg tgc ctctttgtct gcgtgggtca gaagagttgt 1740
gcacgcagat tagcaggcca aggtctgagc cacagcagca tttttatttc agattttgat 1800
aactgtttat atgtgttgaa aaccaaaatg acatctttt aaagcttatc cataaaaaaa 1860
aatagatgtc ttttatagtg gaaaaacaca tggggaaaaa aatcatctat ttgatgcag 1920
catttgataa tgataaaaca cctcacacct cactctttat agtcacaaa atgaatgagg 1980
tctgggctag gtagaaaaag ggtcaatgct atttttgttt ttagaatcat taccttttac 2040
cagcttttaa ccatctgata tctatagtag acacactatc atagttaaca tagttaagtt 2100
cagcacttgt ctcattttaa tgtaaagatt tgcttccatt ttcctacagg cagtctctct 2160
cttctcaca gtcccactgt gcaggtgcta ttgttactct tacgaatatt ttcagtaatg 2220
ttattttctt ctaagtgaat tttctagcct gcactttgat gtcattgtgt ccctttgtct 2280
ttcaaactcc aagggtcccc tgtggccctc tcccttacc tggaaggcc tcttgagac 2340
cttaccctg gctgt ttgga cttgtatata tttaaataat ttaactacc ttaattactt 2400
aaaaaaaaa aaaaaa 2416

```

<210> 382

<211> 378

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(378)

<223> 3' terminal sequence. homeo box a5 (HOXA5) gene.

<400> 382

```

tttttttttt ttgttatagt tacttcaagt aacacagctt gtttcatata aataagttaa 60
aacatctatt ttttttcaag acaaagccat tcaggacaaa gagatgaaca gaaagcagat 120
ctacttatac aggcgcata atggcaataa acaggctcat gattaaaaga tgaattaggg 180
caacgagaac agggcttctt cacagaagga acacaaggga gtttcagaaa gtcaccttag 240
tactgacact acgcgggac cgctaatac tgctcagta tttaaacgct cagatactca 300
gggacggaag gccctccctt gccgcggnc atnctccatg gcttttcagc ttattatc tt 360
ttttccactt caatcncc 378

```

<210> 383

<211> 439

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

242/292

<221> misc_feature
 <222> (1)..(439)
 <223> 5' terminal sequence. homeo box a5 (HOXA5) gene.

<400> 383
 aaatcaagca cacatantan aaaacaaatg agctcttatt ttgtaaactc attttgcggt 60
 cgctatccaa atggcccggg ctaccagttg cataattatg gagatcatag ttccgtganc 120
 gagcaattca gggactcggc gagcatgcac tccggcaggt acggctacgg ctacaatggc 180
 atggatctca gcgtcggcng ctcgngctcc ngcacttttg ctccggagag cgcgcccgc 240
 gctacgtnc aagcgcacgc ggcncactcc aagcccaggt acagcnagcc ggccacgtcc 300
 acgcaactctn cctcanncg atccgctgcn ctgctcgcnc gtngggccct tcgcccngga 360
 ancgacanna ccaanggcgg gaaaaactcc ctttaaggca a ctccagcngg cgcctcgggc 420
 cgacngccgg aagcaccca 439

<210> 384
 <211> 813
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(813)
 <223> homeo box a5 (HOXA5) gene.

<400> 384
 atgagctctt attttgtaaa ctcatcttgc ggtcgtatc caaatggccc ggactaccag 60
 ttgcataatt atggagatca cagttccgtg agcgagcaat tcagggactc ggcgagcatg 120
 cactccggca ggtacggcta cggctacaat ggcatggatc tcagcgtcgg ccgctcgggc 180
 tccggccact ttggctccgg agagcgcgcc cgcagctacg ctgccagcgc cagcgcggcg 240
 cccgccgagc ccagggtacag ccagccggcc acgtccacgc actctcctca gcccgatccg 300
 ctgccctgct ccgccgtggc cccctcgccc ggcagcgaca cgcaccacgg cgggaaaaaac 360
 tccctaagca actccagcgg cgctcggcc gacgccggca gc acccat cagcagcaga 420
 gagggggttg gcacggcgtc cggagccgag gaggacgcc ctgccagcag cgagcaggcg 480
 agtgcgcaga gcgagccgag cccggcgccg cccgcccaac cccagatcta cccctggatg 540
 cgcaagctgc acataagtca tgacaacata ggcggccccg aaggcaaaag ggcccggacg 600
 gcctacacgc gctaccagac cctggagctg gagaaggagt tccacttcaa ccgttacctg 660
 acccgagaaa ggaggattga aatagcacat gctctttgccc tctccgagag acaaattaaa 720
 atctggttcc aaaaccggag aatgaagtgg aaaaaagata ataagctgaa aagcatgagc 780
 atggccgcgg caggaggggc cttccgtccc tga 81 3

<210> 385
 <211> 447
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(447)
 <223> 3' terminal sequence. x-box binding protein 1 (XBP1) gene.

<400> 385

243/292

```

gcattgtacc ttttaattgc atgggtagtt ttaaataaat ggagaaagca ctttcagaa 60
gctacactag caggaaaaaa ttccatcaag catttacata gttaaatttct ataatttcac 120
aaaagattct tgatcttact tgaagtatac atgagggaaa gagccccctc agcaggtggt 180
cccgttgctt acagaagcaa actaaaggac ctaaaactgg aggcaagcca ggatgc caaa 240
aagggggaag agaaatgata aagaaccatt cataaattcc atgtctactt caagacattt 300
gtctaattgac ctttacataa taagtatttt agggaaaact accacccttt taagataaaa 360
gtacaatctt aaaagctgta gttctcaatt atagtaatat ttctacttc cagtaatatg 420
tctcaatacc ttggactgct ggatgtc

```

447

<210> 386
 <211> 462
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(462)
 <223> 5' terminal sequence. x-box binding protein
 1 (XBP1) gene.

```

<400> 386
aagaacctgt agaagatgac ctcgttcgag agctgggtat ctcaaactctg ctttcatcca 60
gccactgccc aaagccatct tctgcctac tggatgctta cagtgcactgt ggatacgggg 120
gttccctttc cccattcagt gacatgtcct ctctgcttgg tgtaaaccat tcttgggagg 180
acacttttgc caatgaactc tttcccca gc tgattagtgt ctaagggaatg atccaatact 240
gttgcccttt tcttgacta ttacactgcc tggaggatag cagagaagcc tgtctgtact 300
tcattcaaaa agccaaaata gagagtatac agtcctagag aattcctcta tttgttcaga 360
tctcatagat gaccccccagg tattgtcttt tgacatccca agcagtccaa ggtattggag 420
acatattact gggaagtaaa gaaatattac tnataattgg ag

```

462

<210> 387
 <211> 1836
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(1836)
 <223> x-box binding protein 1 (XBP1) gene.

```

<400> 387
ggcgtggggc ggctgcggcg cgcggtgcgc ggtgcgtagt ctggagctat ggtggtggtg 60
gcagccgcgc cgaaccggcg cgacgggacc cctaaagttc tgcttctgtc ggggcagccc 120
gcctccgcgc ccgagccccc ggccggccag gccctgccgc tcatggtgcc agcccagaga 180
ggggccagcc cggaggcagc gagcgggggg ctgccccagg cgcgcaagcg acagcgcctc 240
acgcacctga gccccgagga gaaggcgctg aggaggaaaac tgaaaaacag agtagcagct 300
cagactgcca gagatcgaaa gaaggctcga atgagtgagc tggaacagca agtggtgatg 360
ttagaagaag agaaccaaaa acttttgcta gaaaatcagc ttttacgaga gaaaactcat 42 0
ggcctttagt ttgagaacca ggagttaaga cagcgttgg ggatggatgc cctggttgct 480
gaagaggagg cggaagccaa gggaatgaa gtgaggccag tggccgggtc tgctgagtc 540
gcagactca gactacgtgc acctctgcag cagggtgcagg ccagttgtc acccctccag 600
aacatctccc catggattct gccggtattg actcttcaga ttcagagtct gatatactgt 660
tgggcattct ggacaacttg gaccagtc tgttcttcaa atgcccttcc ccagagcctg 720

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ccagcctgga ggagctccca gaggtctacc cagaaggacc cagttcctta ccagcctccc 780
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ttgaccacat atataccaag cccctagtct tagagatacc ctctgagaca gagagccaag 900
ctaattgtgt agtgaaaatc gaggaagcac ctctcagccc ctcagagaat gatcaccctg 960
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gtaagatcaa gaatcttttg tgaaattata gaaatttact atgtaaat gc ttgatggaat 1740
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caattaaaag gtacaatgca aaaaaaaaaa aaaaaa 1836

```

<210> 388

<211> 433

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(433)

<223> 3' terminal sequence. tumor necrosis factor,
alpha-induced protein 3 (TNFAIP3) gene.

<400> 388

```

tttttcttaa ataatttatt ttttaatggt gactcttggtg aaaagttaca tttattttaga 60
aaaacttgaa gaaatccaac aaagaatagg tggctttcta ttaggggacaa ttaaattgtgc 120
aaatttcaaa tactttttat aataagtata aataattact ttttttcaca ttaagaatgg 180
aaataatgat caacacaana tattaagata tcaactttaa gagaattaga tgaaaacact 240
gaagtttatt tngtatcct tggaangaa ttataaagat tcgtctggga aaaactt agg 300
gggctctaag gggaaagttg tgcctaatag tatgagtaaa ggctgtgtag agttatggat 360
cacaaatatt ttcaggccnt aagtacagac ccccnaaatg gcagccttta tcnccgggga 420
aatgcattt ccc 433

```

<210> 389

<211> 206

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(206)

<223> 5' terminal sequence. tumor necrosis factor,
alpha-induced protein 3 (TNFAIP3) gene.

<400> 389

245/292

ctcaaccagc tgccttttta aaggga gctc tagtcctttt tgtgtaattc actttattta 60
ttttattaca aacttcaaga ttatttaagt gaagatatct cttcagctct ggggaaaatg 120
ccacagtgtt ctcttgagag aacatccttg ctttgagtca ggctgtgggc aagttcctga 180
ccacagggag taaattnn cctctt 206

<210> 390

<211> 4426

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4426)

<223> tumor necrosis factor, alpha -induced protein
3 (TNFAIP3) gene.

<400> 390

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agcacaatgg ctgaacaagt cttcctcag gctttgtatt tgagcaatat gcggaaagct 120
gtgaagatac gggagagAAC tccagaagac atttttaaac ctactaatgg gatcattcat 180
catttttaaaa ccatgcacog atacacactg gaaatgttca gaacttgcca gtt ttgtcct 240
cagtttcggg agatcatcca caaagccctc atcgacagaa acatccaggc caccctggaa 300
agccagaaga aactcaactg gtgtcgagaa gtccggaagc ttgtggcgct gaaaacgaac 360
ggtgacggca attgcctcat gcatgccact tctcagtaca tgtggggcgt tcaggacaca 420
gacttggtac tgaggaaggc gctgttcagc a cgctcaagg aaacagacac acgcaacttt 480
aaattccgct ggcaactgga gtctctcaaa tctcaggaat ttgttgaaac ggggctttgc 540
tatgatactc ggaactggaa tgatgaatgg gacaatctta tcaaaatggc ttccacagac 600
acacccatgg cccgaagtgg acttcagtac aactcactgg aagaaatata catatttgc 660
ctttgcaaca tcctcagaag gccaatcatt gtcatttcag aaaaaatgct aagaagtgtg 720
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taaattgtaac ttttcacaag agtcaacatt aaaaaataaa ttattt 4426

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<210> 391

<211> 440

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(440)

<223> 3' terminal sequence. serum response factor
(c-fos serum response element-binding
transcription factor) (SRF) gene.

<400> 391

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ttttttgtg cacaaaaatg atacatttat tgaagagta tttttttttt aatacaaaaag 60
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agtagaaaac actgacatac acactcacat tcaagcacac acactcactc aggcgcacac 180
accacacac acatacccca gagccaccga ggaagggaac caccaagggt cgctgcacat 240
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aacacacatt ataagcactt tgctgatcc actcactngg gtctgtcttt tgtgggaagg 360
agaggaaaga ttcatcaaag gtctctccc catgggtngg gggagtgggg agtgagttag 420
tgatggtgga gtgaacaagg

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440

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<210> 392
<211> 471
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(471)
<223> 5' terminal sequence. serum response factor
(c-fos serum response element-binding
transcription factor) (SRF) gene.

<400> 392
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tgcagcaaag gggagccaga aatgggcagt tctcccaggg agtgagcagc tactgtaact 120
tttttaaat aagacaaaaa gccttgaaga aaatgacttt atttttctaa gtgtaacctc 180
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accacctata tccagaaggg gagctttttc agaaacaggg cagcagtggg gtgaaaat 360
cttaaccctt aagactgcct tcagtaagga acaagctggc ttctgtgatt aggtgaagg 420
atgggggaag attttaatgc acagccta gt tatcaagggg atgatttgcc g 471

<210> 393
<211> 4201
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(4201)
<223> serum response factor (c-fos serum response
element-binding transcription factor) (SRF) gene.

<400> 393
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gtgtgtgtg tgagcgtggc cttgggagga catgcgtgtg tcagggatga gttgaggtga 3960
tatttttatg tgcagcgacc cttgggtgtt cccttctctg gtgctctgg ggtatgtgtg 4020
tgtgggtgtg tgcgcctgag tgagtgtgtg tgcctgaatg tgagtgtgta tgtc agtggg 4080
ttctacttcc cctgggatgc tgaccagga atagtggaca tggtcacagt cctatgtaca 4140
gagctttctt ttgtattaaa aaaaaatact ctttcaataa atgtatcatt tttgtgcaca 4200
g 4201

```

<210> 394

<211> 563

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

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<220>
<221> misc_feature
<222> (1)..(563)
<223> 3' terminal sequence. sry (sex determining
region y)-box 9 (campomelic dysplasia, autosomal
sex-reversal) (SOX9) gene.

<400> 394
tttttaaatgc aatgtatatatt tattgtaaac aataatatac aaaaaaaaaa aagagaaaga 60
aaaagggaaa ggtaagtttc acggagagaa caaaaggttt ggggctggga gggaaacaag 120
tgaacaaaac aaaacacgaa cacaaaccaa agcttttacc taaagacaaa atatgattta 180
aatgccagggt ttccttaagtt acaga agtat ctttttaaaa agatctgctt ttatacagaa 240
attgaaggat gccatattat gagtgcctta agattttatt ctactgactt ctaaaactgt 300
taatatatct ttttttaaat aaaaaaaaaa gtttgctgtc ttttttaaaa agcaatcctc 360
aaactctcta gccacagcag taattaagat taaggctctgt cagtgggctg atccctcca 420
ggtagcctcc ctactccaa gagaagatgc ngagaaatat gggatggaca catgcctgca 480
tgtttttgtg nccaaacaca cacanacca nacacacnca caatataagg cngccccaag 540
gtctntggcc gaaancctgg caa 563

<210> 395
<211> 3936
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3936)
<223> sry (sex determining region y) -box 9
(campomelic dysplasia, autosomal sex -reversal)
(SOX9) gene.

<400> 395
ggagagccga aagcggagct cgaaactgac tggaaacttc agtggcgcgag agactcgcca 60
gtttcaaccc cggaaacttt tctttgcagg aggagaagag aaggggtgca agcgcccca 120
ctttgtctct ttttcctccc ctctcctccc tctccaattc gcctccccc acttgagcgc 180
ggcagctgtg aactggccac cccgcgcctt cctaagtgtc cgccgcggtg gccggc cgac 240
gcgccagctt ccccgggagc cgcttgcctc gcatccgggc agccgagggg agaggagccc 300
gcgctcgag tcccagagcc gccgcggctt ctgcctttc ccggccacca gcccctgcc 360
ccgggcccgc gtatgaatct cctggacccc tcatgaaga tgaccgacga gcaggagaag 420
ggcctgtccg gcgccccag cccacccatg tccg aggaact ccgcgggctc gccctgccc 480
tcgggctccg gtcggacac cgagaacacg cggccccagg agaacacgtt cccaagggc 540
gagccgacg tgaagaagga gagcgaggag gacaagttcc ccgtgtgcat ccgcgagcg 600
gtcagccagg tgctcaaagg ctacgactgg acgctggtgc ccatgccggt gcgcgtcaac 660
ggctccagca agaacaagcc gcacgtcaag cggcccatga acgccttcat ggtgtgggcg 720
caggcgcgcc gcaggaagct cgcggaccag taccgcact tgcacaacgc cgagctcagc 780
aagacgctgg gcaagctctg gagacttctg aacgagagcg agaagcggcc cttcgtggag 840
gaggcgagc ggctgcgct gcagcacaag aaggaccacc cggattacaa gtac cagccg 900
cggcgaggga agtcggtgaa gaacgggcag gcggaggcag aggaggccac ggagcagacg 960
cacatctccc ccaacgcgca cttcaaggcg ctgcaggccg actcgccaca ctctcctcc 1020
ggcatgagcg aggtgcactc ccccggcgag cactcggggc aatcccaggg cccaccgacc 1080
ccaccacca ccccaaaaac cgacgtgcag ccgggcaagg ctgacctgaa gcgagagggg 1140
cgccccttgc cagagggggg cagacagccc cctatcgact tccgcgacgt ggacatcgcc 1200
gagctgagca gcgacgtcat ctccaacatc gagaccttcg atgtcaacga gtttgaccag 1260
tacctgccgc ccaacggcca cccgggggtg ccggccacgc acggccaggt cacctacacg 1320
ggcagctacg gcatcagcag caccgcggcc accccggcga gcgcgggcca cgtgtggatg 1380
tccaagcagc aggcgcggcc gccaccccc cagcagcccc cacaggcccc gccggccccg 1440

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caggcgcccc cgcagccgca ggcggcgccc ccacagcagc cggcggcacc cccgcagcag 1500
ccacaggcgc acacgctgac cacgctgagc agcagagccg gccg gtcccc gcgaacgcac 1560
atcaagacgg agcagctgag cccagaccac tacagcgagc agcagcagca ctgccccaa 1620
cagatcgccct acagcccctt caacctccca cactacagcc cctcctaccc gccatcacc 1680
cgctcacagt acgactacac cgaccaccag aactccagct cctactacag ccacgcggca 1740
ggccagggca cgggcctct a ctccaccttc acctacatga accccgctca gcgccccatg 1800
tacaccccca tcgccgacac ctctggggtc ccttccatcc cgcagacca cagccccag 1860
cactgggaac aaccggtcta cacacagctc actcgacctt gaggaggcct cccacgaagg 1920
gcgacgatgg ccgagatgat cctaaaaata accgaagaaa gagaggacca accagaat tc 1980
cctttggaca tttgtgtttt tttgtttttt tttttgttt tgttttttct tcttcttctt 2040
cttccttaaa gacatttaag ctaaaggcaa ctctgaccca aatttccaag acacaaacat 2100
gacctatcca agcgcatcac ccacttgttg ccaatcagtg gccaggccaa ccttggttaa 2160
atggagcagc gaaatcaacg agaaactgga ct ttttaaac cctcttcaga gcaagcgttg 2220
aggatgatgg agaatcgtgt gatcagtggt ctaaactctc ctgcctgttt ggactttgta 2280
attatttttt tagcagtaat taaagaaaaa agtctctgtt gaggaatatt ctctatttta 2340
aatattttta gtatgtactg tgtatgattc attaccattt tgaggggatt tatacatatt 2400
tttagataaa attaaatgct cttatttttc caacagctaa actactctta gttgaacagt 2460
gtgcccagc ttttcttgca accagagtat tttgttacag atttgcttct tcttacaaa 2520
agaaaaaaa aatcctgttg tattaacatt taaaaacaga atttgtttat gtgatcagtt 2580
ttgggggtta actttgctta attcctcagg ctttgcgatt taagga ggag ctgccttaaa 2640
aaaaaataaa ggccttattt tgcaattatg ggagtaaaaca atagtctaga gaagcatttg 2700
gtaagcttta tgatatatat attttttaaa gaagagaaaa acaccttgag ccttaaaacg 2760
gtgctgctgg gaaacatttg cactctttta gtgcatttcc tctgccttt gcttggtcac 2820
tgcagctta agaaagaggt aaaaggcaag caaaggagat gaaatctgtt ctgggaatgt 2880
ttcagcagcc aataagtgcc cgagcacact gcccccggtt gcctgcctgg gcccatgtg 2940
gaaggcagat gcctgctgc tctgtcacct gtgcctctca gaacaccagc agttaacctt 3000
caagacattc cacttgctaa aattatttat ttgttaagga gaggttttaa ttaaaacaaa 3060
aaaaaattct tttttttttt tttttttcca attttacctt ctttaaaata ggttggttga 3120
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ctacatcttc tcttgagtg agggaggcta cctggagggg atcagcccac tgacagacct 3540
taatcttaat tactgctgtg gctagagagt ttgaggattg ctttttaaaa aagacagcaa 3600
actttttttt ttatttaaaa aaagatatat taacagtttt agaagtcagt agaataaaa 3660
cttaaaagcac tcataatatg gcaccttca atttctgtat aaaagcag at ctttttaaaa 3720
aagatacttc tgtaacttaa gaaacctggc atttaaatca tttttgtct ttaggtaaaa 3780
gctttgggtt gtgttcgtgt tttgtttgtt tcacttggtt cctcccagc cccaaacctt 3840
ttgttctctc cgtgaaactt acctttccct ttctcttctt cttttttttt ttgtatatta 3900
ttgtttacaa taaatatata tt gcattaaa aagaaa 3936

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<210> 396

<211> 204

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(204)

<223> 3' terminal sequence. cadherin 15,
m-cadherin (myotubule) (CDH15) gene.

<400> 396

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tttttttttt tttttttttt tttttttttt ttttttttca ttcagattta cccaggaggt 60
tgctgtcttt canacaaaga tgaggttcac tggaggaggg caaagggtgg actaggaggg 120

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tgaccgcgat gggccagatn ggagagaaac tcttcccacc ccggcagaag gggcctcttc 180
ctggccgccc catccanact cagg 204

<210> 397
<211> 458
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(458)
<223> 5' terminal sequence. cadhe rin 15,
m-cadherin (myotubule) (CDH15) gene.

<400> 397
caggacgcct acgacatcag ccagctgcgt caccgcagag cgctgagcct gcctctggga 60
ccgccgcccac ttccagagaga tgccccgcag ncagcctgca cccccagcca ccccgagtgc 120
tgcccaccag ccccttgagc atcgccgact tcatcaatga tggcttggga g gctgcagata 180
gtgacccacag tgtgcgcct tacgacacag ccctcatcta tgactacgag ggtgacggct 240
cgggtggcggg gacntgagct ccctcctgtc cagccagggc gatgaggacc aggactacga 300
ctacctcaga gactgggggc cccgcttcgc ccggctggca gacatgtatg ggcacccgtg 360
cgggttngga gttacggggc cagatgg gac caccaggcca gggagggctt ttctcctggg 420
gcactgctac ccagacacag aggccggaca gcctgan 458

<210> 398
<211> 2833
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2833)
<223> cadherin 15, m-cadherin (myotubule) (CDH15)
gene.

<400> 398
acttgcgctg tcactcagcc tggacgcgct tcttcgggtc gcggtgcac tccggcccg 60
ctcccgcctc ggccccgatg gacgcgcgct tctcctcgt cctcgggctg ttggcccaga 120
gcctctgcct gtctttgggg gtt cctggat ggaggaggcc caccaccctg taccctggc 180
gccgggcgccc tgccctgagc cgcgtgcgga gggcctgggt catccccccg atcagcgtat 240
ccgagaacca caagcgtctc ccctaccccc tggttcagat caagtcggac aagcagcagc 300
tgggcagcgt catctacagc atccaggac ccggcgtgga tgaggagccc cggggcgctt 360
tctctatcga caagttcaca gggaaggtct tctcaatgc catgctggac cgcgagaaga 420
ctgatcgctt caggctaaga gcgtttgccc tggacctggg aggatccacc ctggaggacc 480
ccacggacct ggagattgta gttgtggatc agaatacaca ccggccagcc ttcctgcagg 540
aggcgttcac tggccgcgtg ctggagggtg cagtcaccag cac ctatgtg accagggcag 600
aggccacaga tgccgacgac ccgagacgg acaacgcagc gctgcggttc tccatcctgc 660
agcagggcag ccccgagctc ttcagcatcg acgagctcac aggagagatc cgcacagtgc 720
aagtggggct ggaccgcgag gtggtcgcgg tgtacaatct gacctgcag gtggcggaca 780
tgtctggaga cggcctcaca g ccaactgcct cagccatcat cacccttgat gacatcaatg 840
acaatgcccc cgagttcacc agggatgagt tcttcatgga ggccatagag gccgtcagcg 900
gagtggatgt gggacgcctg gaagtggagg acagggacct gccaggctcc ccaaactggg 960
tggccagggt caccatcctg gaaggcgacc ccgatgggca gttcaccatc cgcacggacc 102 0

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ccaagaccaa cgagggtgtt ctgtccattg tgaaggccct ggactatgag agctgtgaac 1080
actacgaact caaagtgtcg gtgcagaatg agggcccgtc gcaggcggct gcccttaggg 1140
ctgagcgggg ccaggccaag gtccgcgtgc atgtgcagga caccaacgag cccccgtgt 1200
tccaggagaa cccacttcgg accagcctag cagagggg gc acccccaggc actctggtgg 1260
ccacctttct tccccgggac cctgacacag agcagctgca gaggctcagc tactccaagg 1320
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acgtgctcag cccggcgtcc cccttcctca agggcggtcg gtacagagcc atcgtcctgg 1440
cccaggatga cg cctcccag ccccgaccg ccaccggcac cctgtccatc gagatcctgg 1500
agggtgaacga ccattgcacct gtgctggccc cgccgcgccc gggcagcctg tgcagcgagc 1560
cacaccaagg cccaggcctc ctctctggcg ccacggatga ggacctgccc cccacgggg 1620
cccccttcca cttccagctg agccccaggc tcccagagct cggccggaac t ggagcctca 1680
gccaggtcaa cgtgagccac gcgcgcctgc ggccgcgaca ccaggtcccc gaaggcctgc 1740
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tgaacgtgac cgtgtgccgc tgcggcaagg acggcgtctg cctgccgggg gccgcagcgc 1860
tgctggcggg gggcacaggc ctgagc ctgg gcgcactggt catcgtgctg gccagcggccc 1920
tcctgtctgt ggtgctgtgc ctgctcgtgg cactccgggc gcggttctgg aagcagtctc 1980
ggggcaaggg gctgctgcac ggcccccagg acgaccttcg agacaatgtc ctcaactacg 2040
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cgacagcgtc gagcctgcct ctgggacgcg cgccacttcg cagagatgcc ccgcagggcc 2160
gcctgcaccc ccagccaccc cgagtgtgct ccaccagccc cctggacatc gccgacttca 2220
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gaccctgggg cgca actgga catgccactc ccgggcctcg tggcagtgat ggccctgca 2580
gaggcagcct gaggtcaccc ggcccagccc ccctgggcct ggggcagcct ccttcctgta 2640
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ccttcctgcc ggggtgggaa gagtttctct ccacggccc catgcgggtc acc tccctag 2760
tccaccttt gcctcctacc agtgaacctc atctttgtat gaaagacagc aacctcctgg 2820
gtaaatctga atg 2833

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<210> 399

<211> 646

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> misc_feature

<222> (1)..(646)

<223> 3' terminal sequence. b-cell cll/lymphoma 2
(BCL2) gene.

<400> 399

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tatctcacac tgtactttat ttttcttcac aatattaact agacagacaa ggaaagttta 60
atggcaatgt gactttttcc aacaacacaa acaaagtgcc attata gcta atggtggcca 120
actggagact tactttacct taaccatgta aagtatcctt accgtatttt ttatgtgtac 180
agtgttgcag aatatcagcc acctcttaaa agtatcaatc ttaaaaagag ccatggaagg 240
taaaagtatg aaaatcttga taacaaaagc tttcaatata aaaacactta ttgtacactt 300
atthttattht aaacaaaaaa taac cccagt aactcaaaac aaaagcaaac cttggttgaa 360
aacttaagaa ggtataataa acaaaaccac caaaagaaag cttccccaaa agaatgcaa 420
tccactgtca ctcttgcaaa ttctaccttg gagggaaaaa ctaaatgaaa tgagctatct 480
ggagggccca cggagatttt ccaaaagggt taggtgcatt gatthtactca gtatctacnt 540
acagtcttat ttattaatag ctgaganttc ctgattgagc gagcctttcc atctccacca 600
gtgtcccccac ttctgtgcnc acttgggntg cagacacctt gtgttg 646

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<210> 400
<211> 465
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(465)
<223> 5' terminal sequence. b-cell cll/lymphoma 2
(BCL2) gene.

<400> 400
ggtattttaa caataaatgt gcagttttta ctaacaggat atttaatgac aaccttctgg 60
ttggtaggga catctgtttc taaatgttta ttatgtacaa tacagaaaa aattttataa 1 20
aattaagcaa tgtgaaactg aattggagag tgataataca agtcctttag tcttaccag 180
tgaatcattc tgttccatgt ctttggacaa ccatgacctt ggacaatcat gaaatatgca 240
tctcactgga tgcaaagaaa atcagatgga gcatgaatgg tactgtaccg gttcatctgg 300
actgccccag aaaaataact tcaagcaaac atcctatcaa caacaagggtt gttctgcata 360
ccaagctgag cacagaagat gggaacactg gtggaggatg gaaaggctcg ctcaatcaag 420
aaaattctga gactattaat aaataagact gtagtgtaga tactg 465

<210> 401
<211> 419
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(419)
<223> 3' terminal sequence. ests (EST W73386)
gene.

<400> 401
gaaggtcatt ctgcgatgg gtttattgca ggagatgatg gaccaaattg ctctgacaca 60
tgacacagct cctgggcacg cctgctgcgn gtncgcttcc catga ccccc agggccctct 120
atgcctcccc ccagggcac cctgccact tgccccact tcatgtacca ccaagccctt 180
tccttttctg ggcaccactc ctgagcagcg tgaccagcgg cctccaagtg catgtggctc 240
agaacataaa agcatcttca acattcgtca ttgagccaaa cgaaacacag tgtttggtc 300
aagagccggc gacactngca tcc ctatcca cacgtggaac ctgcccttgg gcttngttga 360
ccggaggatn ggcgcgtctt ccttgtcatc cagcanccgg agcatgtatg tgcccaga 419

<210> 402
<211> 568
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(568)
<223> 3' terminal sequence. granzyme a (granzyme

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1, cytotoxic t-lymphocyte-associated serine
esterase 3) (GZMA) gene.

<400> 402
tcatgcaaat tgattttatt tgtgaaaaga ttaagaagcc acagtanatg aaaggaaacg 60
gttattttaa ctgctccctt gatagt cata attatccagt tgaggtgttt ctttgagaga 120
agaatataga caccaggccc acgaggggtct ccgcatttat tttcaaggcc aaaggaaagt 180
accctcgga aaacaccctc gcacaacaaa gggcttccag aatctccatt gcacgagtct 240
cttccacctc ggaggtcttc agcacaaccc atattcattc caatcacagg gttaaaatta 300
tagtgatttc gatcattgca gactttctg tctatgatgg gtgatattga ctgcactca 360
gagtatcggg acccaagatg cactattggg gagtctgcc ccaccctggc aacttggcac 420
atggttctct gntttcacat caatccccct ttttagggag atgaaggata gtcacatatn 480
tggttatttt ggctttttcc ggtcagctgt aaagttttaa ggtccc ctnc gcgtttggtg 540
gggcctagcc tgggagggga aanccttt 568

<210> 403
<211> 878
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(878)
<223> granzyme a (granzyme 1, cytotoxic
t-lymphocyte-associated serine esterase 3) (GZMA)
gene.

<400> 403
cagattttca ggttgattga tgtgggacag cagccacaat gaggaactcc tatagatttc 60
tggcatcttc tctctcagtt gtcgtttctc tctgtctaatt tctgaagat gtctgtgaaa 120
aaattattgg aggaaatgaa gtaactcttc attcaagacc ctacatggc ctacttagtc 180
ttgacagaaa aaccatctgt gctggggctt tgattgcaaa agactgggtg ttgactgcag 240
ctcactgtaa cttgaacaaa aggtcccagg tcattcttgg ggctcactca ataaccaggg 300
aagagccaac aaaacagata atgcttgta agaaagagtt tcc ctatcca tgctatgacc 360
cagccacacg cgaagggtgac cttaaacttt tacagctgac ggaaaaagca aaaattaaca 420
aatatgtgac tatccttcat ctacctaaaa agggggatga tgtgaaacca ggaaccatgt 480
gccaagtgc aggtggggg aggaactcaca atagtgcac ttggtccgat actctgagag 540
aagtcaatat caccatcata gacagaaaag tctgcaatga tcgaaatcac tataatttta 600
accctgtgat tggaatgaat atggtttgtg ctggaagcct ccgaggtgga agagactcgt 660
gcaatggaga ttctggaagc ctttgttgt gcgaggtgt tttccgagg gtcacttct 720
ttggccttga aaataaatgc ggagaccctc gtgggcctgg tgtctatatt cttctctcaa 780
agaaacacct caactggata attatgacta tcaaggagc agtttaaata accgtttct 840
ttcatttact gtggttctt aatcttttca caataaaa 878

<210> 404
<211> 191
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(191)
<223> 3' terminal sequence. v-fos fbj murine

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osteosarcoma viral oncogene homolog (FOS) gene.

<400> 404

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gcagtgaccg tgctcctacc cagctctgct tcacagcgcc cacctgtctc cgcccctcgg 60
cccctcgccc ggccttgcta accgccacga t gatgttctc gggcttcaac gcagactacg 120
aggcgtcadc ctcccgtgc agcagcgcg t ccccgccgg gataaactct ctttattaca 180
attaatcanc g 191
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<210> 405

<211> 245

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(245)

<223> 5' terminal sequence. v-fos fbj murine
osteosarcoma viral oncogene homolog (FOS) gene.

<400> 405

```
ttttcaactt aaatgctttt attgacaatg tcttgaaca ataagcaaac aatgcttaaa 60
tttttcattc aaattcactt tccacatgtc aaaagaccto aaggtagaaa aaaataaaat 120
aaaaatataa atatctgaga atccatctta ataaataaat taaaaacaca ataaaacgtt 180
ttcatggaaa actgttaatg tccngaacat tcagaccacc tcnacaatgn gtgntcngtn 240
anatt 245
```

<210> 406

<211> 489

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(489)

<223> 3' terminal sequence. interleukin enhancer
binding factor 1 (ILF1) gene.

<400> 406

```
gcgncgcgct caccgaagg ngnangtaga cagcgggtca gaggccgcct agagccggag 60
gacaccccaa atacaaacat accacggaga gacctgggat ctgagtttca aaagggcctg 120
tgataaaaga ctgaatcttt ttccaaatga agtagaaatg gttctgtcgt tttaaacata 180
cacaataactt aggagacttg tt ttactcag agtggaataat tttgccaggg acaaagtcaa 240
cacaagaaaa caaacaacaa aaaatagcca gaaagagaac agttaagtgc agctcgggtga 300
gtcccggcag ttccttcccg gcactggctc gtccctgggt tctcaagggt ccatgcggcc 360
acagcgtccg tccacctgtc caccgagcc acatgctgaa atgggagggt ggataaaatt 420
catcaggcag ctgctgtaac acggaaatgt gcagatgcca gagtagcttc gtctgaactt 480
gaacaagac 489
```

<210> 407

<211> 247

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(247)

<223> 5' terminal sequence. interleukin enhancer
binding factor 1 (ILF1) gene.

<400> 407

```
tggttttcagc ctatggaatg atttcctttt gtctgtcttg ttcaagttca gacgaagcta 60
ctctggcatc tgcacatttc cgtgttacag cagctgcctg atgaa tttta tccacctcca 120
tttcagcatg tggctcgcgt ggacagggtg acggacgctg tggccgcatg gaaccttgag 180
aaccagggga cgagccagtg ccgggaagga actgccggga ctcaccganc tgcncctaac 240
tggtctc                                     247
```

<210> 408

<211> 3059

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3059)

<223> interleukin enhancer binding factor 1 (ILF1)
gene.

<400> 408

```
gcccccccc cagcctcct cccctcctcc cgcccgcgcg tgctcccgcc cctcgccgcc 60
gctcgctcgc tcgccggcgc gctccgctc ggccccctcc ctacgctccg gtgcgcggcg 120
gccgacgacc cgcgccctgg gctccggcgc gccaccggcg ccgcgcggga gcggcccggg 180
ggccctcagc caggcccatg gcggcggcgc ggcgcgctct cgggccgggc accacgcggg 240
cgcgggggcg ggggcgcgg ggcgggggcg ggtcccgccg ggcgctgggc cgtgggcccgc 300
ctggagggcc gcgagttcga gtatctgatg aagaagcgct cggtgaccat cgcccgcaac 360
tcgtcgcagg gctcggtgga cgtgagcatg ggccactcga gttcatctc ccggcgccac 420
ctcgagatct tcacgcccc gggcggcgcg gccatggcgc ggccgctccg gagctgccgc 480
ccgcgcagcc caggcccgac gcggcggcgc acttctacct gcgctgcttg ggcaagaacg 540
gggtattcgt ggacggcgctg ttccagaggc gcggggcgcc gccgctgcag ctgccgcgcg 600
tgtgcacatt caggttcccg agcacaaca tcaagataac gttcactgcc ctgtccagcg 660
agaagagaga gaagcaggag gcgtctgagt ctccagtga a ggccgtacag ccacacatct 720
cgcccccgac catcaacatt ccagacacca tggcccacct catcagccct ctgccctccc 780
ccacgggaac catcagcgct gcaaactcct gcccctccag cccccgggga gcggggtctt 840
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agcctgaaaa tgaaaag gaa gcttcagggtg gagacagccc gaaggatgat tcaaagccgc 960
cttactccta cgcgcgctg atagttcagg cgattacgat ggctcccgac aaacagctca 1020
ccctgaacgg gatttataca cacatcata aaaattatcc ctactacagg actgcggaca 1080
agggtggcca gaattcaatt cgccacaatc tctctctgaa tcgttatttc atcaaag tgc 1140
cgcgttccca ggaagaacca ggcaagggt cgttctggag gatagacca gcctctgaaa 1200
gcaaattaat agaacaggct tttaggaaac gacggcctag ggcgctgccc tgctttagaa 1260
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agcggcagct accacaggcc atcaagcctg tcacctacac tgtggccacc ccagtgacca 1560
cctcgacctc ccagccaccc gtcgtgcaga cggttcacgt cgtccaccag atccagcgg 1620
tgtcggtcac cagtgtggcc ggactggccc cagcgaacac gtacactgtc tctggacaag 1680
```

257/292

```
ctgtggtcac cccggcagcc gtgctggccc ctccaaagc agaggcccag gagaatggag 1740
accacagggg agtcaaagt aaagtagagc ctattcccgc cattg gccac gccacgctcg 1800
gcaactgccag ccggatcatt cagacggcac agaccacccc ggtccagacg gtgaccatag 1860
tacaacagggc acctctaggt caacaccagc taccaataaa aactgtaaca caaaacggca 1920
ctcacgtggc atcagtcgcc actgcggtcc acggccaggt gaacaatgcc gcggcgagtc 1980
ctttgcacat gttggcaaca cagcatccg catcgccctc cctgccaca aagcgccaca 2040
acggtgacca gccggagcag ccggagctga agcggatcaa gacagaagac ggcgagggca 2100
tcgtcattgc cctgagcgtg gacacgccac cggcagccgt aagggaaaag ggtgtccaga 2160
actagcgacc gggagagctt tcttttaacg atatcaactc tgtggtgcc aaggagac g 2220
cggcctcccc ccagcactcg ggggtgcagg gccctgtggt tggacttcac ctctcagcac 2280
tgaaaaccca aaaccagct ggccttaaca ctccctaaag acagaagtca cactgaaca 2340
aaaccacac acaacaaaac ctgatttggg agacggtgtc tccactgagc acctgctggg 2400
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ggactcaccg agctgcactt aactgttctc tttctggcta tttttgttg tttgtttctt 3000
tgtgttgact ttgtccctgg caaaattttc cactctgagt aaaacaagtc tcggaattc 3059
```

<210> 409

<211> 201

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(201)

<223> 3' terminal sequence. rho gdp dissociation
inhibitor (gdi) alpha (ARHGDIA) gene.

<400> 409

```
tttttttttt tccttcaggg gcattttattt cccggtcaga aaagaagcag ggacaggcgc 60
ctctgcctga gcctggcaga cacaacacga agaccgggga tggggcgggg gaggcacagg 120
agacggctct cagcaatgtg tgcacttggt cccttgtttg ttctggctg ggtcagggaa 180
ggcctgccgn ggggtggtggc a 201
```

<210> 410

<211> 297

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(297)

<223> 5' terminal sequence. rho gdp dissociation
inhibitor (gdi) alpha (ARHGDIA) gene.

<400> 410

258/292

ggcctctgct gccctttctg tgccccccag gttctatctc cccgtcacac ccgaggcctg 60
gcttcaggag ggagcggana gccattctcc agggcccggtg gttgcccctg gacgtgtgcg 120
tctgctgctc cggggtggan ctgggggtgtg ggatgcacgg cctcgtgggg gccggggcgt 180
cctccagccc cgctgctccc tggccagccc cc ttgtcgct gtcggtcccg tctaaccatg 240
atgccttaac atgtggagtg tacctgtggg gcctcactaa gcctctaant cactgtg 297

<210> 411

<211> 1819

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1819)

<223> rho gdp dissociation inhibitor (gdi) alpha
(ARHGDI A) gene.

<400> 411

cctgaaccgc ggggccgaac cctccgggtg cccgaccag gctaagcttg agcatggctg 60
agcaggagcc cacagccgag cagctggccc agattgcagc ggagaacgag gaggatgagc 120
actcgggtcaa ctacaagccc ccggcccaga agagcatcca ggagatccag gagctggaca 180
aggacgacga gagcctgcga aagtacaagg aggccctgct gggccgcgtg gccgtttccg 240
cagaccccaa cgtccccaac gtctgtgtga ctggcctgac cctggtgtgc agctcggccc 300
cgggcccctt ggagctggac ctgacgggag acctggagag cttcaagaag cagtcgtttg 36 0
tgtctgaagga ggggtgtggag taccggataa aaatctcttt ccgggttaac cgagagatag 420
tgtccggcat gaagtacatc cagcatacgt acaggaaagg cgtcaagatt gacaagactg 480
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acgacgacaa gaccgaccac ctgtcctggg agtggaaatc caccatcaag aaggactgga 660
aggactgagc ccagccagag gcgggcaggg cagagtgtat gacggaagac ggacaggcgg 720
atgtgtcccc ccagcccct cccctcccca taccaagggt ctgagcaggc cctccgtgcc 780
cctccaccct ggtccgcct c cctggcctgg ctcaaccgag tgctccgac cccctcctc 840
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cctcactagc ctctactccc tgtgtctgca tgagc atgtg gcctccccgt cccttccccg 1260
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ggggaagcga aaattgccaa cactcaagtc acctcagtag catccaggag gctgggtatt 1440
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ccctcgatgg acaggcctga cccacccac ctggggccag ccaggagccc cgcctggggc 1560
atcagtattt attgcctccg tccgtgccgt ccctgggcca ctggctggcg cctcttcccc 1620
cagcctctca gtgccaccac ccccggcagc cttccctgac ccagccagg a caaacaaggg 1680
accaagtgtg cacattgtgt agagcgtct cctataggtc ccccgcccca tccccgtgt 1740
tggtgtgtgt tctgccagga tcaggcagag gcgcctgtcc ctgcttcttt tctgaccggg 1800
aaataaatgc ccctgaagg 1819

<210> 412

<211> 306

<212> DNA

<213> Artificial Sequence

<220>

259/292

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(306)

<223> 3' terminal sequence. complement component

4a (C4A) gene.

<400> 412

```
gctgccaaaa gcctttaata tgccctggtc ccaggctgt g ttcattgaaag cggacacagc 60
agtgtctcca gcttcatggt tcccagggtc aggttctctc cagcggaggt gggagggcag 120
ccctcacacc tggcaccctt gactgcatac tcttgaggga agtcgttgag ctggggcacag 180
gctgcccgtt ggcgggttgc tccggcacag gcgttcagag ggcattctct cgatccagct 240
attcgagtcc agcaagta ct ngggggggnc cctcccaggg gcataantng gncntccag 300
anccat 306
```

<210> 413

<211> 5417

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5417)

<223> complement component 4a (C4A) gene.

<400> 413

```
agaaggtagc agacagacag acggatctaa cctctcttgg atcctccagc catgaggctg 60
ctctgggggc tgatctgggc atccagcttc ttcaccttat ctctgcagaa gccaggttg 120
ctcttgttct ctcttctgtt ggttcatctg ggg gtcccc tatcgggtgg ggtgcagctc 180
caggatgtgc cccgaggaca ggtagtgaag ggatcagtg tcttgagaaa cccatctcgt 240
aataatgtcc cctgtctccc aaagggtggc ttcaccctta gctcagaaag agacttcgca 300
ctcctcagtc tccaggtgac cttgaaagat gcgaagagct gtggcctcca tcaactcctc 360
agaggccctg aggtccagct ggtggcccat tcgcatggc taaaggactc tctgtccaga 420
acgacaaaac tccagggtat caacctgtc ttctctctc gccgggggca cctctttttg 480
cagacggacc agcccattta caacctggc cagcgggttc ggtaccgggt ctttgcctcg 540
gatcagaaga tgcgcccag cactgacacc atcacagtca tgggtggaga ctc tcacggc 600
ctccgcgtgc ggaagaagga ggtgtacatg ccctcgtcca tcttcagga tgactttgtg 660
atcccagaca tctcagagcc agggacctg aagatctcag cccgattctc agatggcctg 720
gaatccaaca gcagcaccga gtttgagtg aagaaatag tccctcccaa ctttgagggtg 780
aagatcacc ctggaaagcc ctacatctg a cgggtgccag gccatcttga tgaaatgcag 840
ttagacatcc aggccaggta catctatggg aagccagtgc aggggtggc atatgtgcgc 900
tttgggctcc tagatgagga tggtaagaag actttcttcc gggggctgga gactcagacc 960
aagctgggtg atggacagag ccacatttcc ctctcaaagg cagagttcca ggacgcctg 1020
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cattactact acatgatcct atcccaggg cagatcgtgt tcatgaatcg agagcccaag 1620
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gtggccttct actaccatgg agaccacca gtggccaact cctgcgagt ggatgtccag 1740
gctggggcct gcgagggcaa gctggagctc agcgtggagc gtgccaagca gtaccggaac 1800
```

260/292

ggggagtcg tgaagctcca cttagaaacc gactccctag ccttgggtggc gctgggagcc 1860
ttggacacag ctctgtatgc tgcaggcagc aagtc caca agcccctcaa catgggcaag 1920
gtctttgaag ctatgaacag ctatgacctc ggctgtggtc ctgggggttg ggacagtgc 1980
cttcagggtg tccaggcagc gggcctggcc ttttctgatg gagaccagtg gaccttatoc 2040
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gatccattgg acactttagg cctctgtcac caggaggcgt ggcctccctc 3060
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gggctgggtc agccggccag cgcaaccc tg tacgactact acaacccga gcgcagatgt 4740
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aaagtgtcag tgttggc 5417

<210> 414
<211> 408
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(408)
<223> 3' terminal sequence. cd3g antigen, gamma
polypeptide (tit3 complex) (CD3G) gene.

<400> 414
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tatttgagaa acccccaa at ttgctctgat ggcttttctt ctccatttgt catctctggg 120
aaccttgagt ctagatttag ggctgaaagt ctctctgcta ggagctttcc aaaatgcatt 180
gttttgattc tgggaactga ataggaggag aacacctgga ctactctgag tctgagttc 240
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<210> 415
<211> 457
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(457)
<223> 5' terminal sequence. cd3g antigen, gamma
polypeptide (tit3 complex) (CD3G) gene.

<400> 415
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gcagaagcca aaaatatcac atggtttaaa gatgggaaga tgatoggctt cctaactgaa 120
gataaaaaaa aatggaatct gggaagtaat gccaaggacc ctgagggat gtatcagtgt 180
aaaggatcac agaacaagtc aaaaccactc caagtgtatt acagaatgtg tcagantgc 240
attgaactaa atgcagccac catatctggc tttctctttg ctgaaatcgt cagcatttct 300
gtccttgctt ttggggtcta cttcattgct ggacaggatg gag ttcgcca gtcgagagct 360
tcagacaagc agactctgtt gcccaatgac cagctctacc agccctcaa ggatccgagg 420
aagatgacca gtacagccac cttcaagggn aaccagt 457

<210> 416
<211> 822
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature

262/292

<222> (1)..(822)

<223> cd3g antigen, gamma polypeptide (tit3 complex) (CD3G) gene.

<400> 416

```
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<210> 417

<211> 439

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(439)

<223> 3' terminal sequence. v-rel avian
reticuloendotheliosis viral oncogene homolog b
(nuclear factor of kappa light polypeptide gene
enhancer in b-cells 3) (RELB) gene.

<400> 417

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aggggatggg ggtgctagac atcctgggtt gggattgcac ggctcctcca cctcctccc 360
caccagtgcc cctcctctg gcacgcggg gctacgtggc ttcaggcccg gggataggag 420
gccgccccca aaggccgct 43 9
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<210> 418

<211> 234

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(234)

<223> 5' terminal sequence. v-rel avian
reticuloendotheliosis viral oncogene homolog b

263/292

(nuclear factor of kappa light polypeptide gene
enhancer in b-cells 3) (RELB) gene.

<400> 418

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acgggggatg cccaacgtcc ttggggagct gaacagtctg gaccccatg gcatcgagag 60
caaacggcgg aagaaaaagc cggccatcct ggaccacttc ctgcccaacc acggctcagg 120
cccgttcctc ccgccgtcag ccctgctgcc agaccctgac ttcttctctg ggcaccgtgt 180
tccctgcccg gcngggaggc cctggggggc ctgnacctcc tgggacgatg gggt      234
```

<210> 419

<211> 2314

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2314)

<223> v-rel avian reticuloendotheliosis viral
oncogene homolog b (nuclear factor of kappa light
polypeptide gene enhancer in b-cells 3) (RELB)
gene.

<400> 419

```
ggaattcccc ccgggcccg ccccgcgccc cgcagc cccg ggcggcgcgc gtctgccccg 60
gcctgcggcc cagcccttgc gccgctcgtc cgaccgcgga tcgtccacca gaccgtgcct 120
cccgcccgcc cgggccccgc gtgcatgctt cggctctggc cagcctctgg gccgtccgtc 180
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 gtttttgagc ctcaaaaaaa aaaaaaggaa ttcc 2314

<210> 420

<211> 214

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(214)

<223> 3' terminal sequence. estrogen receptor 1
 (ESR1) gene.

<400> 420

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 acaaagcaaa gctgcgacaa aaccgagtc catcagtaat agtatgcac ggcaaaagg 180
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<210> 421

<211> 520

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(520)

<223> 5' terminal sequence. estrogen receptor 1
 (ESR1) gene.

<400> 421

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 agcgtaatt atgctctgtt tccaactgca tttcctttcc aattgaa tta aagtgtggcc 120
 tcgttttttag tcatttaaaa ttgttttcta agtaattgct gcctctatta tggcacttca 180
 attttgact gtcttttgag attcaagaaa aatttctatt ctttttttg catccaattg 240
 tgcctgaact tttaaaatat gtaaatgctg ccatgttcca aaccatcgt cagtgtgtgt 300
 gttagagct gtcaccctag aaaca acata ttgtcccatg agcaggtgcc tgagacacag 360
 acccctttgc attcacagag aggtcattgg ttatagagac ttgaattaat aagtacatt 420
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 cagtgtagag ctcttgtttt atgggaaaag gctcaaatgc 520

<210> 422

<211> 6450

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(6450)
<223> estrogen receptor 1 (ESR1) gene.

<400> 422
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266/292

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<210> 423

<211> 580

<212> DNA

<213> Artificial Sequence

267/292

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(580)

<223> 3' terminal sequence. pre -b-cell leukemia
transcription factor 1 (PBX1) gene.

<400> 423

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gaggcacagg ggcagggaag atgacgaaaa ccaggctgac agctggaggc agggaagggt 180
ggcttctacc cagaaaaaaa aggggagaga gtataaagaa gtgtccagat tggctgaaat 240
agcatcccaa agaagagaag agaaggagac tcttattgtg ttgc tgatt gcttcgacct 300
ccagtctgac cgcttcaggc ttgggagaga aaccctccct tctgcccct gccccaactg 360
ggcgacaggg tcagccggga tgcgattgct gggagatcag ttggaggat cagagtgaac 420
actgccaggg ccttctgtag gggaggtcac tgatgaagg gtagtagcat cctgccaacc 480
tccattagca ctgatgccct gcg gactgta catctgactg gctgcgagtc catcactgta 540
tcctcctgtc tggctgataa catggcgaag ggtatccacc 580
```

<210> 424

<211> 503

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(503)

<223> 5' terminal sequence. pre -b-cell leukemia
transcription factor 1 (PBX1) gene.

<400> 424

```
gccaaagagg agttagccaa gaagtgtggc accacagtct cccaggtatc acaactggtt 60
tggaataaag cgaatccggt acaagaagaa cataggtaaa tttcaagagg aagccaatat 120
ttatgtctgcc aaaacagctg tcaactgctac caatgtgtca gcccatggaa gccaaagctaa 180
ctcgccctca actcccaact cggctggtgg atacccttgc ccatgttatc agccagacag 240
gaggatacac tgatggactc gcagccagtc agatgtacag tccgcaggca tcagtgtctaa 300
tggagggttg caggatgcta ctacccttc atcagtgacc t cccctacag aaggccctgg 360
cagtgttcac tctgatacct ccaactgac tcccagcaat cgcaccccg ctgaccctgt 420
gcccagttg ggcaggggca ggaggaggg tttctctccc aacgctgaag cggtcagact 480
ggagggtcaaa cgattaggca aac 503
```

<210> 425

<211> 1819

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1819)

<223> pre-b-cell leukemia transcription factor 1
(PBX1) gene.

268/292

<400> 425

```

cttccctgtt tatcctgaaa aggatttgaa g acaagcttg aaggataaaa agccttggtg 60
cttcccagga gccgagccga ggagcagaag aggaagagcc gggggctgcc gtagcctttg 120
gagatggacg agcagcccag gctgatgcat tcccatgctg gggtcgggat ggccggacac 180
cccggcctgt ccagcactt gcagatggg gccggaggga ccgaggggga gggcgggagg 240
aagcaggaca ttggagacat tttacagcaa attatgacca tcacagacca gagtttggat 300
gaggcgcagg ccagaaaaca tgctttaaac tgccacagaa tgaagcctgc cttgtttaat 360
gtgttggtgt aaatcaaaga aaaaacagtt ttgagtatcc gaggagccca ggaggaggaa 420
cccacagacc ccagctgat gcggctggac aacatgctgt tagcggaagg cg tggcgggg 480
cctgagaagg gcggaggggc ggcggcagcg gcggcagcgg cgggcgcttc tggaggggca 540
ggttcagaca actcagtga gcattcagat tacagagcca aactctcaca gatcagacaa 600
atctaccata cggagctgga gaaatacagc aggcctgca acgagttcac caccacgtg 660
atgaatctcc tgcgagagca aagccggacc aggccatct ccccaaagga gattgagcgg 720
atggtcagca tcatccaccg caagttcagc tccatccaga tgcagctcaa gcagagcacg 780
tgcgaggcgg tgatgatcct gcgttcccga tttctggatg cgcgggcgaa gagacggaat 840
ttcaacaagc aagcgacaga aatcctgaat gaatatttct attcccatct cagcaaccct 900
taccacgtg aggaagccaa agaggagtta gccaaagaat gtggcatcac agtctcccag 960
gtatcaaact ggtttggaaa taagcgaatc cgttacaaga agaacatagg taaatttcaa 1020
gaggaagcca atatttatgc tgccaaaaca gctgtcactg ctaccaatgt gtcagcccat 1080
ggaagccaaag ctaactcgcc ctcaactccc aactcggctg gttcttcca g ttttttaac 1140
atgtcaaact ctggagattt gttcatgagc gtgcagtcac tcaatgggga ttcttaccaa 1200
ggggcccagg ttggagccaa cgtgcaatca cagggtggata cccttcgcca tgttatcagc 1260
cagacaggag gatacagtga tggactcgca gccagtcaga tgtacagtcc gcagggcatc 1320
agtgtaatg gaggttgga gga tgctact accccttcat cagtgaacct ccctacagaa 1380
ggccctggca gtgttcactc tgatacctcc aactgatctc ccagcaatcg catcccggct 1440
gaccctctgc ccagttggg gcaggggcag gagggagggt ttctctccca agctgaagcg 1500
gtcagactgg aggtcgaaag aatcagcaaa cacaataaga gtctccttct cttctcttct 15 60
ttgggatgct atttcagcca atctggacac ttctttatac tctcttccct ttttttctg 1620
ggtagaagcc acccttccct gcctccagct gtcagcctgg tttctgcat cttccctgcc 1680
cctgtgcctc tgtcctagac ttcccggggc ccccgccctc tctcatatca ctgaaggata 1740
ttttcaacaa ttagaggaat ttaaagagga aaaaaat tac aaagaaaata ataaaagtgt 1800
ttgtacgttt tcaaaaaaa 1819

```

<210> 426

<211> 506

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(506)

<223> 3' terminal sequence. gli -kruppel family

member gli3 (greig cephalopolysyndactyly syndrome)

(GLI3) gene.

<400> 426

```

taaaaagagg gtggtttgag tgtaacaata ctgattcaaa actgaaatgg aagacagttt 60
ctccctagaa tactttaggg tttttcagag tccttttcca taaa aggaat ataattgaaa 120
cacatctcag ttaggtgaga tgagattgct aaaatacata cagaactaaa aaaacagcca 180
aaacaaagtc agtttaatct cttcaactcc taatgatttc cggtgggtgc agtctttttt 240
tcctaaagcc tattgcataa ctgcaaggga attgctttct tccgctaggg aggtcagcaa 300
agaactcatg tccccgatag cc atgttggt ggtgctcatg gacagcgctg ggaatgggag 360
ggacgcccga gggctggtta aagccggaag aaactatgga aaagggtctca atgatacttg 420
ggctcagggc cccgacatca ggctcgagtg gtcccatct ctatgattgc atcgaagtca 480
atctggtacc ctcccaggcc aggctg 506

```

<210> 427
 <211> 239
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(239)
 <223> 5' terminal sequence. gli -kruppel family
 member gli3 (greig cephalopolysyndactyly syndr ome)
 (GLI3) gene.

<400> 427
 ggcagaagga tcacttgagg ccaggcattc aagaccagcc tatgcaagat aatgagacct 60
 tgtctctatt taaaaaacia aaagcctggt gtgggtggtgc atgcctgtag tctcagcctc 120
 ctgagtagct gggactataa gcacgcacca ctatgtctgg ctaatttttg tatttttagt 180
 agagacaggg tttcaccacg ttgcccaggg cagtcttgaa ctctgaccc caagtgatc 239

<210> 428
 <211> 5054
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(5054)
 <223> gli-kruppel family member gli3 (greig
 cephalopolysyndactyly syndrome) (GLI3) gene.

<400> 428
 cgatactacg tgggcatttt tggctgaaga gagctgaagt aatgagaaga catcatggag 60
 gccagtgccc acagctccac gaccactgaa aagaaaaaag ttgagaattc catagtgaag 120
 tgtccactc gaacagatgt gacgagaaa gccgttgctt ccagcaccac ttctaagag 180
 gatgaaagtc ctggacagac ttatcacaga gagagaagaa acgcaatcac tatgcagcca 240
 cagaatgtcc aggggctcag caaagtcagt gaggaacctt caacatcgag tgacgagagg 300
 gcctcattga tcaagaaaga gatccatggg tccctgccac acgtggcgga gccctctgtg 360
 ccgtaccgag ggacgggtg tt tgccatggac ccaggaatg gttacatgga gcccactac 420
 caccctctc atcttttccc tgccttccat cctctgtac caattgatgc cagacatcat 480
 gagggccggt accattacga tccatctccg attctc

cat tgcatatgac ttccgcctta 540
 tctagtagcc ctacgtatcc ggacctgccc ttcattagga tctccccaca ccggaacc cc 600
 gctgtgctt ccgagtctcc ctccagccct ccacatccct acattaatcc ctacatggac 660
 tatatccgct ccttgacacag cagcccatcg ctctccatga tctcagcaac ccgtgggctg 720
 agccctacag atgcgccccca tgcaggagtc agcccagcag aatactatca tcagatggcc 780
 ctgctaactg gccagcgcag cccctatgca gacatt attc cctcagctgc caccgcccgc 840
 acggggggcca tccacatgga atatcttcat gctatggata gcaccagatt ctccagcccc 900
 aggtgtcag ccaggccgag ccgaaaacgt acactgtcca tatcaccact ctccgatcat 960
 agctttgacc ttcagacat gataaggacg tctcccaact ccttggtcac gattctcaat 1020
 aattcccgta gcagctcttc agcaagtggc tcctatggtc acttatctgc aagtgaate 1080
 agccctgcct tgagcttcac ctactcttc gcgcccgtct ctctccacat gcatcagcag 1140
 atctaagcc gacaacagag cttaggttca gcctttggac acagccctcc actcatccac 1200
 cctgcccaca cttttccaac acagaggcct attccagga tccctacggt tc tgaacccc 1260

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gtccagggtca gctccggccc ttctgagtc tccacagaaca agcccacgag tgagtctgca 1320
 gtgagcagca ctgggtgaccc gatgcacaac aagagggtcca agatcaaacc cगतgaagac 1380
 ctccccagcc caggggctcg ggggcagcag gaacagcccg aaggaacaac ccttgtcaag 1440
 gaggaagggg acaaaagatga aagcaaa cag gagcctgaag tcatctatga gacaaactgc 1500
 cactgggaag gctgcgcgag ggagttcgac acccaagagc agcttgtgca ccatataaat 1560
 aacgaccata ttcatggaga gaagaaggag ttctgtgtgca ggtggctgga ctgctcaaga 1620
 gagcagaaac ccttcaaagc ccagtatatg ttggtagtgc atatgagaag acacacgggc 1680
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 tgcaacaagg cttttctaaa tgcctctgat cgcgccaaac accaaaacag aacgcattcc 1860
 aatgagaaac catatgtgtg caaaatoccca ggctgcacta agcgttacac agaccaagc 1920
 tccctccgga aacatgtgaa gacagtgcac ggcccagagg ctcatgtcac caagaagcag 1980
 cgaggggaca tccatcctcg gccgccaccg ccgagagatt ccggcagcca ttacagtc 2040
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 tctcagccaa gccctgggtg tcagtcttca tgcagcagcc aacagtcccc catcagcaac 2220
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 acgccccgc ccaacatgga gaggatgagc ctgaagacgc gcctggcgct gctcgggat 2940
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 aacccctga ggagcgggccc tgctgggggc tctcagacc tcggggagaa cagcaacccc 3720
 tacgggtggc cagagcactt gatgctccac aacagccccc gaagtggcac cagtggaaac 3780
 gccttccatg aacagccctg taaggcccc cagtatggga actgtctcaa caggcagcca 3840
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 agcaccacca tgcaagggag cgggggccag ctgaatttcg gcctgccggt agcgcctaat 3960
 gagtacgtg gcagcatggt gaatggcatg cagaaccagg acccagtggt acaggggtac 4020
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 cagatgctg ggcagattag tgctacctca cacatcaaca tctaccaagg gccagagagc 4140
 tgctgccag gggctcacgg catgggcagc cagccgtcaa gcttggcagt tgtcaggggc 4200
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 gctctgagc caggacagc t cagtgcacac agtcagacct gcagggtgaa tggatatcaag 4320
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 tcagacgcca gctctgct acaggggacc agcgcctaaa actctgagtt actttccc ca 4500
 ggtgctaatc aggtgacaag cacagtggac agcctcgaca gccatgacct ggaaggggta 4560
 cagattgact tcgatgcat catagacgat ggggaccact ccagcctgat gtcgggggccc 4620
 ctgagcccaa gtatcattca gaacctttcc catagctcct cccgcctcac cagcctcgg 4680
 gcgtccctcc cattcccagc gctgtccatg ag caccacca acatggctat cggggacatg 4740
 agttctttgc tgacctccct agcgggaagaa agcaaatcc ttgcagttat gcaataggct 4800
 ttaggaaaaa aagactgcaa ccaacggaaa tcaataggag ttgaagagat taaactgact 4860
 ttgttttggc tgttttttta gttctgtatg tatttttagca atctcatctc acctactga 4920

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gatgtgtttc aattatatc cttttatgga aaaggactct gaaaaaccct aaagtattct 4980
aggagagaaac tgtcttccat ttcagttttg aatcagtatt gttacactca aaccaccctc 5040
tttttaaaaa aaaa 5054

<210> 429
<211> 271
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(271)
<223> 3' terminal sequence. interleukin enhancer
binding factor 1 (ILF1) gene.

<400> 429
aggagacttg ttttactcag agtggaaaaat ttgcccaggg acaaagtc aa cacaaagaaa 60
caaacaacaa aaaatagcca gaaagagAAC agttaagtgc agctcgggtga gtcccggcag 120
ttccttcccg gcaactggctc gtccctgggt tctcaagggtt ccatgcggcc acagcgtccg 180
tccacctgtc cagcgagcc acatgctgaa atggagggtg ataaaattca tcaggcagct 240
gctgtaacac ggaaatgtgc agatgcc aga g 271

<210> 430
<211> 193
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(193)
<223> 5' terminal sequence. Similar to Retinoblastoma -like protein 2,
sw|Q08999|RBL2_HUMAN.

<400> 430
TGTCTACATT TNCCACATA AAAATGAAAC AATNNTTCT CCTCGNGAAA AGATTTTATA 60
TTACTTNAGC NAAAGTCCTT CAAAGNGACT GAGCGNANNT AATAGTNTGA TACGCATAGG 120
NGNAACTCCT ACTNNAANGN GCGGNNTTCT TNTNGNNGAT GGCNGTGAAT NCACTGCAAA 180
NAGCATTTGC CCN 193

<210> 431
<211> 184
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(184)
<223> 3' terminal sequence. Homo sapiens CD2 antigen (p50).

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<400> 431
AGTCAAAGCT TTTATTTCAC TTTNACTCAC AGGATGGGGG GCAAGTNTCC ACCAGGGCAC 60
ATAAGAACT CCAGAGTCTC TTAAGCAGAT AGGCTGCTTG TAGNGAGACC CAGGNACACC 120
AATCACTTGA TTTATCGCAT CTACACATGA CCNGAGAGGG GACAAGAAAT CTCTAAGTTT 180
TCTG 184

<210> 432
<211> 242
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(242)
<223> 5' terminal sequence. Similar t o NM_022641 Homo sapiens
chorionic somatomammotropin hormone 1 (placental lactogen) (CSH1

<400> 432
ATTCGGCAGC ATGACTGGCC AGGGTATAAA AAGGGCCCAC AAGAGACCGG CTCTAGGATC 60
CCAAGGCCCA ACTCCCCGAA CCACTCAGGG TCCTGTGGCA GCTCACCTAG TGGCAATGGC 120
TCCAGGCTCC CGGAACGTCC CTGATCCTGG NTTTTGNCCT NCTCTNACTG CCCTGGNTTN 180
AANAAGCTNG TGCCNTCCAA ANCGTTCCGT TATCCAGGGT TTTTGACCAC GCTATGCTNC 240
AA 242

<210> 433
<211> 329
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(329)
<223> 5' terminal sequence. Homo sapiens plasminogen activator (PLAT)

<400> 433
AACAGTCACC GACAACATGC TGTGTGCTGG AGACACTCGG AGCGGCGGGC CCCAGGNAAA 60
CTTGACGAC GCCTGCCAGG GNATTTGCGG AGGCCCCCTG GTGTGTCTGA ACGATGGCCG 120
CATGACTTTG GTGGGCATCA TCAGCTGGGG CCTGGGCTNT GGACAGAAGG ATGTCCCGGG 180
TGTGTACACC AAGGTTACCA ACTACCTAGA CTGGATTCTG GACAACATGC GACCGTGACC 240
AGGAACACCC GACTCCTCAA AAGNAAATGA GATCCCGNCT CTTCTTCTTC AG AAGACACT 300
GCAAAGGCGC AGTGCTTCTC TACAGACTT 329

<210> 434
<211> 247
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature

273/292

<222> (1)..(247)

<223> 3' terminal sequence. Homo sapiens plasminogen activator (PLAT)

<400> 434

```
AAATATATCT GAANNNTTA AGTACAGTNT AAAACAGGGT TNTGGCAACA GAAAGTAAAA 60
ACTAACATGG NTTGCTATAA ATATGCTGAA GCCTAGTTGT TCAAATGATA CAATTCTCTC 120
ATGCTACTCT AAAGTTTNTA AAGNAAAAGG GTTTACACTT TACACACT GT ACACAAAGGG 180
GNTACCTTCT GNGNGCCNGG GAGTGGGGAA AGGGGANGGN GACTTGACGT CAAGGGTGCT 240
TTTGAGG                                     247
```

<210> 435

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(63)

<223> 5' terminal sequence. Homo sapiens aminoacylase 1 (ACY1).

<400> 435

```
CCGCCAGNAC CTGCGTATCC GCACTGTTCA GCCCAAGCCT GACTATGGAG CTGCTGTGGC 60
TTT                                     63
```

<210> 436

<211> 190

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(190)

<223> 3' terminal sequence. Homo sapiens aminoacylase 1 (ACY1).

<400> 436

```
GAAGAGGAGG NCCTTGGCAC TGGTNGGGAN GGAAGCCCCA GGGGAAAAGG TTNAGGAGTC 60
CCAGGGCTCA GCTGTCAC TG CAGGGGCAG GCACACTGGC AGGGCCAGGC AGCAGGCNNG 120
TATATATGNC CACCCACGG AGGAACACAG CCTNATGCAG NCGTTNATCG TGGTNGTGCA 180
GNAGCACAGG                                     190
```

<210> 437

<211> 176

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(176)

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<223> 3' terminal sequence. Homo sapiens E74 -like factor 1 (ets domain transcription factor) (ELF1)

<400> 437

CCCTTAGGCT GTTCTGGTGA TGAGGCTCCC GGTGAGTCTG CATATTTTNN TTGCACCTGC 60
TGTGTTTCCA TCACTTCAGG AATCCCATCT AATGTGACGG ACACATGGGT GACTGGGGCA 120
ACAACCATGT CATCTTCAGG NGAACATAAT ATATTATTAT TTATCCGGTT TTCATC 176

<210> 438

<211> 465

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(465)

<223> 5' terminal sequence. Homo sapiens selectin P,
granule membrane protein CD62, SELP

<400> 438

NGGAACATAT GGAGTTTTTA CA AACGCTGC ATTTGACCCG AGTCCTTAAG AGACCTGTCC 60
TTTTCTGGT CTCCTCATTC AGCCTCCATA TGATCCTGTT GTGAACATCA AGTTTCCTGC 120
TACACTGGAC TTAACATATA TGCATTGCT GCAGGTTTCC ATAAACACCC ATGANTCAAA 180
GACATGGAAT TACCTTAGAT TAGCTCTGGA CCAGCCTGTT GGACCCGCTC TGGACCAACC 240
CTGTTTCCTG AGTTTGGGAT TGTGGTACAA TCTCAAATTC TCAACCTACC ACCCCTTCCT 300
GTCCACCTC TTCTCTCCT GTAACACAAG CCACAGAAGC CAGGAGCAAA TGTTTCTGCA 360
GTAGTCTCTG TGCTTTGACT CACCTGTAC TTGAAATACC AGTGAACCAA AGAGACTGGA 420
GCATCTGGAC TTNACAAGAA GACCAGACTT GTGGAGANAT TAA AA 465

<210> 439

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(396)

<223> 3' terminal sequence. Homo sapiens selectin P,
granule membrane protein CD62, SELP

<400> 439

GAAAATCCTT TNAATTACGN ATTTNAANAT TGGNCTTTGG GNCATTTGAG GGACAGTGAC 60
TGGGGGCAGG AAGGCCACAG GNGACATGTG GCCTTCTAGC TTATNCTTG GCCTTCTGCA 120
GCCTCTGGGG CCATCCAGAG GACTCTCTGG AAGCCTCAGA GCAGAGGNCC AAGAGGCCTC 180
ATCAACAGCA ACCANTGGAG ACTCCAGAAG ATGCTACAGG ANTTNCTCCC AATTAGAGAT 240
GCCACCTGTT TNCCAACAAA GTGGAGAAAA CCTTCCTNNA ATCAAAAANT AAAGAGGTNT 300
TTCNATTTCT CCACAGTTTG GCCTCCTTGT GAGTCAGATG NTCCAGTCTC TTTGGNNCAC 360
TGGTATTTC AATAACAGGT GAGNNAAGG ANAGAG 39 6

<210> 440

<211> 337

<212> DNA

275/292

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(337)

<223> 5' terminal sequence. Human interleukin 3 receptor (hIL -3Ra).

<400> 440

```
AAAGGCTCAG CAGTTGAC CT GGGACCTTAA CAGAAATGTG ACCGATATCG AGTGTGTTAA 60
AGACGCCGAC TATTCTATGC CGGCAGTGAA CAATAGCTAT TGCCAGTTTG GAGCAATTC 120
CTTATGTGAA GTGACCAACT ACACCGTCCG AGTGGCCAAC CCCCATTCT CCACGTGGAT 180
CCTCTTCCCT GAGAACAGTG GGAAGCCTTT GGCAGGTGCG GAGAATCTGA CCTGCTNGAT 240
TCATGACGTT GATTCTTGA GCTGCAGCTG GCGGGTAGGG CNCGGGGCC CGCGGGACGT 300
CCAGTACGAC CTGTACTTGA ACGTTNCCAA CAGGNGT 337
```

<210> 441

<211> 104

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:prim er

<220>

<221> misc_feature

<222> (1)..(104)

<223> 3' terminal sequence. Human interleukin 3 receptor (hIL -3Ra).

<400> 441

```
TTCCCGCCTC CCAGACCACC AGNTTGNCGT TTTGGNAGNT NTNACCGANG GGGTNTTNCA 60
TGTNAGGGNT NCGGGNAAAN AGTTTNTGAA NCACCAGAAA CCTT 104
```

<210> 442

<211> 223

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(223)

<223> 5' terminal sequence. Human tumor protein p53 (Li -Fraumeni syndrome) (TP53)

<400> 442

```
AAGCAATGGA TGATTGATG CTGTCCCCGG ACGATATTGA ACAATGGTTC ACTGAAGACC 60
CAGGTCCAGA TGAAGCTCCC AGAATGCCAG AGNTGNCTCC CCGCGTGGCC CCTGCACCAG 120
CAGCTCCTAC ACCGGCNGCC CCTGCACCAG CCCCCTCCTG GCCCCTGTCA TCTTCTGTCC 180
CTTCCCAGAN AACCTACCAG GGCAGCTACG GTTTCCTCT G GG 223
```

<210> 443

276/292

<211> 223
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(223)
<223> 5' terminal sequence. Tumor protein p53
(Li-Fraumeni syndrome) (TP53) gene.

<400> 443
aagcaatgga tgatttgatg ctgtccccgg acgatattga acaatgggtc actgaagacc 60
caggtccaga tgaagctccc agaatgccag agntgntcc ccgctgggcc cctgcaccag 120
cagctcctac accggcngcc cctgcaccag cccctcctg gccctgtca tcttctgtcc 180
cttccagaa aacctaccag ggcagctacg gttccgtct ggg

<210> 444
<211> 343
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(343)
<223> 3' terminal sequence.

<220>
<221> misc_feature
<222> (1)..(343)
<223> v-erb-b2 avian erythroblastic leukemia viral
oncogene homolog 2 (neuro/glioblastoma derived
oncogene homolog) (ERBB2) gene.

<400> 444
caaggggctg caaactnncc cacacatgac cccagccctc tacagcggta cagtgaggac 60
cccacagtac ccctgccctc tgagactgat ggctacgttg ccccctgac ctgcagcccc 120
cagcctgaat atgtgaacca gccagatgtt cggccccagc ccccttcgcc ccgagaggcc 180
ctctgcctgc tgcccgaact gctggtgcc ctctggaaag gcccaagact ctctccccag 240
ggaagaatgg ggtcgtcaaa gagtttttgc cttt gggggt gccgtgggag aaccccgagt 300
attgaccccc caggggaggg agcttgccct tcagccccac ctt 343

<210> 445
<211> 309
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(309)
<223> 3' terminal séquence.

<220>
<221> misc_feature
<222> (1)..(309)
<223> zinc finger protein 144 (Mel -18) (ZNF144) gene.

<400> 445
ccgcccccca cccccaaggt gganagagct ggggaaagta gaagaggtgg aaaaaagggc 60
ccagaaaaag tggaaggagt ggagaggctt ag ctggaaga agggagaggg tccctggcct 120
caagttaagg ggggcacggg agcgccnttg acagtcattc tgcgccccct gctggtngaa 180
ganggtttct tcaggcagtt caagctaccc ccgttngcan ctttngnngc cccacttgct 240
ntcgaagggg ganttgggna ngtagggtn gtngettgan gcccatngga actnggaaaa 300
ccatnggat 309

<210> 446
<211> 268
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(268)
<223> 3' terminal sequence.

<220>
<221> misc_feature
<222> (1)..(268)
<223> MAP/microtubule affinity-regulating kinase 3
(MARK3) gene.

<400> 446
attatcttgt gaatctactt agaaaaacac acacaagcaa tgttcacaac tataaattta 60
aaccttttgc actaaaaaaa cacaaaacaa caaacacaa accacaggca tgaactgtaa 120
acctgtatta actntgaact ggtcttaagg ttaattctta gngtcattc agtatittcc 180
tccttggaac ctgtaatgtt ttngcaccgg ntgatctccc gnggggggta ctagtaatga 240
ctggctgccc gtgtaggag atgcttcc 268

<210> 447
<211> 169
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(169)
<223> 5' terminal sequence.

<220>
<221> misc_feature
<222> (1)..(169)
<223> MAP/microtubule affinity-regulating kinase 3
(MARK3) gene.

<400> 447

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gaacactgat ggaaatgtat agaataatat ttaggcaata acgtctgcat cttctaaatc 60
 atgaaattaa agtctgagga cgagagcacg nctgggngcg aaantntgcc tttttntac 120
 ggatgcacta cantaaagan gtgcanccta tncgncccct gccctactt 169

<210> 448
 <211> 393
 <212> ADN
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(393)
 <223> 3' terminal sequence.

<220>
 <221> misc_feature
 <222> (1)..(393)
 <223> EST N68536 MAX-interacting protein 1 (MXI1) gene.

<400> 448
 aagtaattaa gggtagttaa attatttaaa gtatacaaag tccaaacagc caggggtaag 60
 gtctccaaga ggccttccca gggtaaggga gagggccaca agggaacctt ggagtttgaa 120
 agacaaaggg aacacatgac atcaaagtgc aggctagaaa ttctacttag aagaaaataa 1 80
 cattactgaa aatattcgta agagtaacaa tagcacatgc acagtgggac tgtgaggaag 240
 agagagactg cctgtaggaa aatggaagca aatctttaca ttaaaatgag acaagtgctg 300
 aacttactat gttaactatg atagtgtgtc tacnatagat atcncgatgg ttaaagctg 360
 gtaaaaggta atggttctca aaaccnaaa a tag 393

<210> 449
 <211> 217
 <212> ADN
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(217)
 <223> 5' terminal sequence.

<220>
 <221> misc_feature
 <222> (1)..(217)
 <223> EST R81126 lymphotoxin beta receptor (LTBR) gene.

<400> 449
 ttacntgggt atctcctact gtagtatgag gaagaatggc tgtaaatgta ttttttgaat 60
 tctggnctca cctttgtctc agctaaatgt agccgcatcc gggacacagt ttgtgccaca 120
 tgtgccgaga attcctacaa cgagc actgg aactacctga ccattctgcca nctgtgccgc 180
 ccctgtgacc cagtgatggg cctcgnctga gantgcc 217

<210> 450
 <211> 157
 <212> ADN

279/292

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(157)

<223> 5' terminal sequence

<220>

<221> misc_feature

<222> (1)..(157)

<223> (POU2F2) gene.

<400> 450

nattcggcaa cngggaagg aaagaaacta accaacaaaa gagaaaacca aaaataatca 60
caacagaaac cagctgcccc aaaggaggcc agtngtnggg acgcagaggg tcc tcagagc 120
aggagtnaca agggaggaaa gaccaaaaaa acaacca 157

<210> 451

<211> 282

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(282)

<223> 5' terminal sequence.

<220>

<221> misc_feature

<222> (1)..(282)

<223> caspase 4, apoptosis-related cysteine protease
(CASP4) (ex CASP1)

<400> 451

gagaatctga cagccaggga tatggagtca gcgctgaggg catttgctac cagaccagag 60
cacaagtcct ctgacagcac attcttggtg ctcatgtctc atggcatcct ggagggaatc 120
tgcggaactg tgcgatgatg gaaaaaacca gatgtgctgc tttatgacac catcttccag 180
atattcaaca accgcaactt gcctcagtct ngaaggacaa acccaaggtc atcattgtnc 240
agggtcttgc gaggtgcaa accttggggg aantttggg tc 282

<210> 452

<211> 424

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(424)

<223> 5' terminal sequence

280/292

<220>
<221> misc_feature
<222> (1)..(424)
<223> syndecan 1 (SDC1) (ex HRB)

<400> 452
ttgcttttng caaaactota cttaatccaa tnggtttttc cctgtacagt agattttcca 60
aatgtaataa actttaatat aaagtagtcc tgtgaatgcc actgccttcg cttcttgcc 120
ctgtgctgtg tgtgacgtga ccggactttt ctgcaaacac caacatgttg ggaaacttgg 180
ctcgaatctc tgtgccttcg tctttcccat ggggagggga ttctgggtcc agggtcctc 240
tgtgtatttg cttttttgtt ttggctgaaa ttctcctgga ngtcggtagg ttcagccaag 300
gttttataag ggctgatgtc aatttncgtg gtttgccaan ttccaagccc catcttncta 360
aatgggcaaa aggaaggtgg gatgggcccc agcnacagct ttgnaccc ga gggctnttgg 420
gtca 424

<210> 453
<211> 435
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(435)
<223> 5' terminal sequence

<220>
<221> misc_feature
<222> (1)..(435)
<223> Integrin, beta 2 (antigen CD18 (p95), lymphocyte
function-associated antigen 1; macrophage antigen
1 (mac-1) beta subunit) (ITGB2)

<400> 453
aggagtgtccc cggctgcccc tcaccct gtg gcaagtacat ctctgctgcc gaggtcctga 60
agttcgaaaa gggccctnt ggaagaactg cagcgcgccg tgtccgggcc tgcagctgtc 120
gaacaacccc gtgaagggca ggacctgcaa ggagagggac tcagagggct gctgggtggc 180
ctacacgtg gagcagcagg acgggatgga ccgctacctc atctatgttg atgagagccg 240
agagtgtgtg gcaggcccca acatcgccgc catcgctcggg ggcaccgttg gcaggcatcg 300
tgctgatcgg cattctcctg ctggtcatct gggaaggctc tgatccacct gagcgacctc 360
cgggagttac aggcgttttg agnaggagaa gctcaagtcc cagtnggaac aatgattatt 420
ccctttttca agagc 435

<210> 454
<211> 544
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(544)

281/292

<223> 5' terminal sequence

<220>

<221> misc_feature

<222> (1)..(544)

<223> Protein phosphatase 1, catalytic subunit, alpha
isoform (PPP1CA) (ex MGST1)

<400> 454

```
gtgtgaccag acatgcaacc gncatctatg gtttctacgn atgnagtgnc aagcagnacg 60
nctnacaaca tcaaaactgtg gnaaaacctt cactgnactg ncttcaactg ncctgnccca 1 20
tcgcggncca tagtggacgt aaaagatctt ctgnctgncc acggaggcct gttccccgga 180
cctgncagtt ctatggnagc agattcggcg ggatcatgcg gccacacagat gtgtcctgta 240
ccaggggcct gctgtgtgac ctgctgtggt ctgaccctga caaggacgtg cagggctggg 300
gcgagaacga ccgtgggcgt ctcttttac c tttggagccg aggtggtggc caagttcctc 360
cacaagcacg acttggaact catctgccga gcacaccagg ttgtagaaga cggctacgag 420
ttctttgccg agcggcantt ggtgacactt ttctcagctt ccaactactg ttgcgagttt 480
nacaatgctt gcgccatgat gagtgtgacg agaccctatg tgcttttcag atcttaagcc 54 0
gccn 544
```

<210> 455

<211> 344

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(344)

<223> 3' terminal sequence

<220>

<221> misc_feature

<222> (1)..(344)

<223> protein phosphatase 2 (formerly 2A), catalytic
subunit,alpha isoform (PPP2CA)

<400> 455

```
actgcggtga gagccagcgg ccagcgccac cncaacagcc gccagaagna cagaggaac 60
cgcgcgccgc gngtgcgngt aggcccgtn gcggtgncgg cgcgggagga gccggannca 120
gccggcnggg gcgggnggca ncanggacga gaaggngnnc accaaggagc tggaccagng 180
gaacgagcag cngaacgagn gcaagcagcn gnccgagncc caggncaga gccncagcga 240
gaangcnaaa gaaanccnga caaaagaanc caacnggcaa gaggnncgan gnccagnnac 30 0
ngnccgngga gangngcang ggcaannnca ngaacccatg gaac 344
```

<210> 456

<211> 514

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(514)

<223> 5' terminal sequence

<220>
<221> misc_feature
<222> (1)..(514)
<223> S100 calcium-binding protein A11 (calgizzarin)
(S100A11)

<400> 456
cagcctcccg cgcctcgctc agctccaaca tggcaaaaat ctccagccct acagagactg 60
agcgggtgcat cgagtccttg attgctgtct tccagaagta tgctggaa ag gatgggtata 120
actacactct ctccaagaca gagttcctaa gcttcatgaa tacagaacta gctgccttca 180
caaagaacca gaaggaccct ggtgtccttg accgcatgat gaagaaactg gacaccaaca 240
gtgatgggtca gctagatttc tcagaatttc ttaatctgat tgggtggccta gctatggctt 300
gccatggact ccttcctcaa ggctgtccct tcccagaagc gggacctgga gggaccctt 360
gggcctctggg cctttcaaac ccaccccctn ttcctttcca gcctttctgt tcatcatnnt 420
ccacagccca cccttncctg gaggcacatt aaccacctna tggtagggtn ccaactggtc 480
attagttatt aaaggnaatg tnaatttttt ttaa 514

<210> 457
<211> 359
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(359)
<223> 5' terminal sequence

<220>
<221> misc_feature
<222> (1)..(359)
<223> Granzyme A (granzyme 1, cytotoxic
T-lymphocyte-associated serine esterase 3) (GZMA)

<400> 457
gctggacgtc atcaacaagc attcattcaa caacttccgc ctgcgagtgg ggttgaacca 60
tggaaccgta gtagctggag ttattggggc ccagaagccg caatatgaca tttggggcaa 120
cacagtgaac gtggccagcc gcatggagag tacaggagtc cttggcaaaa tccaagtgaac 180
tgaggagaca gcatggggccc tacagtcctt gggctacacc tgctacagcc nggggtgtca 240
tcanggtgaa aggcaaaggg cagctctgca cctacttcct gaacacagac ttgacacgaa 300
ctggacctcc ttcagctacc ctaggctgag attgcactcg cct tncctaag aacctnaat 359

<210> 458
<211> 1251
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1251)
<223> 3' terminal sequence

<220>

283/292

<221> misc_feature

<222> (1)..(1251)

<223> endothelin 1 (EDN1)

<400> 458

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ggagctgttt acccccactc taataggggt tcaatataaa aagccggcag agagctgtcc 60
aagtcagacg cgccctctgca tctgcgccag gcgaacgggt cctgcgcctc ctgcagtccc 120
agctctccac caccgccgcg tgcgcctgca gacgtccgc tcgctgcctt ctctcctggc 180
agggcgctgcc ttttctcccc gttaaagggc acttgggctg aaggatcgct ttgagatctg 240
aggaacccgc agcgctttga gggacctgaa gctgtttttc ttcgttttcc tttgggttca 300
gtttgaacgg gaggtttttg atcccttttt ttcagaatgg attatttgct catgattttc 360
tctctgctgt ttgtggcttg ccaaggagct cc agaaacag cagtcttagg cgctgagctc 420
agcgcggtgg gtgagaacgg cggggagaaa cccactccca gtccaccctg gcggctccgc 480
cgggtccaagc gctgctcctg ctgctccctg atggataaag agtgtgtcta cttctgccac 540
ctggacatca tttgggtcaa cactcccag caggttggtc cgtatggact tggaagccct 600
aggtccaaga gagccttgga gaatttactt ccacaaaagg caacagaccg tgagaataga 660
tgccaatgtg ctagccaaaa agacaagaag tgctggaatt tttgccaagc aggaaaagaa 720
ctcagggctg aagacattat ggagaaagac tggaataatc ataagaaagg aaaagactgt 780
tccaagcttg ggaaaaagtg tatttatcag cag ttagtga gaggaagaaa aatcagaaga 840
agttcagagg aacacctaag acaaaccagg tcggagacca tgagaaacag cgtcaaatca 900
tcttttcatg atcccaagct gaaaggcaag ccctccagag agcgttatgt gaccacaac 960
cgagcacatt ggtgacagac ttccggggcct gtctgaagcc atagcctcca cggagagccc 1020
tgtggccgag tctgcactct ccaccctggc tgggatcaga gcaggagcat cctctgctgg 1080
ttcctgactg gcaaaggacc agcgtcctcg ttcaaaacat tccaagaaag gttaaggagt 1140
tcccccaacc atcttctactg gcttccatca gtgtaactg ctttgggtctc ttctttcatc 1200
tggggatgac aatggacctc tcagcagaaa caca cagtca cattcgaatt c 1251
```

<210> 459

<211> 2145

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2145)

<223> 3' terminal séquence

<220>

<221> misc_feature

<222> (1)..(2145)

<223> Protein tyrosine phosphatase, non -receptor type 6
(PTPN6)

<400> 459

```
cggcagaact gggaccaccg ggggtgggtg ggcggcccgg cactgggagc tgcattctgag 60
gcttagtccc tgagctctct gcctgccag actagctgca cctcctcatt ccctgcgccc 120
ccttctctct cggaa gcccc caggatggtg aggtggtttc accgagacct cagtgggctg 180
gatgcagaga ccctgctcaa gggccgaggt gtccacggta gcttctctggc tcggcccagt 240
cgcaagaacc aggggtgactt ctgctctctc gtccaggggtg gggatcaggt gaccatatt 300
cggatccaga actcagggga tttctatgac ctgtatggag gggagaagt t tgcgactctg 360
acagagctgg tggagtacta cactcagcag caggggtgtg tgcaggaccg cgacggcacc 420
atcatccacc tcaagtacct gctgaactgc tccgatccca ctagttagag gtggtacct 480
ggccacatgt ctggcgggca ggcagagacg ctgctgcagg ccaagggcga gccctggacg 540
tttcttgtgc gtgaga gcct cagccagcct ggagacttgc tgctttctgt gctcagtgac 600
cagcccaagg ctggcccagg ctccccgctc agggtcaccc acatcaaggt catgtgcgag 660
ggtggacgct acacagtggg tggtttgagg accttcgaca gcctcacgga cctgggtggag 720
```

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```

catttcaaga agacggggat tgaggaggcc tcagggcgct ttgtctacct gcggcagccg 780
tactatgcc aaggggtgaa tgcggctgac attgagaacc gagggttga actgaacaag 840
aagcaggagt ccaggatac agccaaggct ggcttctggg aggagttga gagtttgag 900
aagcaggagg tgaagaactt gcaccagcgt ctggaagggc aacggccaga gaacaagggc 960
aagaaccgct acaagaa cat tctcccctt gaccacagcc gaggatcct gcagggacgg 1020
gacagtaaca tcccgggtc cgactacatc aatgccaaact acatcaagaa ccagctgcta 1080
ggcctgatg agaacgctaa gacctacatc gccagccagg gctgtctgga ggccacggtc 1140
aatgacttct ggcagatggc gtggcaggag aacagccgtg tcactgcat gaccaccga 1200
gagggtggaga aaggccggaa caaatgcgtc ccatactggc ccgaggtggg catgcagcgt 1260
gcttatgggc cctactctgt gaccaactgc ggggagcatg acacaaccga atacaaactc 1320
cgtaccttac aggtctcccc gctggacaat ggagacctga ttcgggagat ctggcattac 1380
cagtacctga gctggccc ga ccatggggtc cccagtgagc ctgggggtgt cctcagcttc 1440
ctggaccaga tcaaccagcg gcaggaaagt ctgcctcagc cagggcccat catcgtgcac 1500
tgcagcgccg gcacggccg cacaggcacc atcattgtca tcgacatgct catggagaac 1560
atctccacca agggcctgga ctgtgacatt gacatccaga agaccatcca g atggcgcg 1620
gcgcagcgct cgggcatggt gcagacggag gcgcagtaca agttcatcta cgtggccatc 1680
gcccagttca ttgaaaccac taagaagaag ctggaggtcc tgcagtcgca gaagggccag 1740
gagtcggagt acgggaacat cacctatccc ccagccatga agaatgccca tgccaaggcc 1800
tcccgcacct cgtccaaac a caaggaggat gtgtatgaga acctgcacac taagaacaag 1860
agggaggaga aagtgaagaa gcagcgggtca gcagacaagg agaagagcaa gggttccctc 1920
aagagggaagt gagcgggtgct gtcctcaggt ggccatgcct cagccctgac cctgtggaag 1980
catttcgcga tggacagact cacaacctga acctaggagt gcccattct tt tgtaattt 2040
aaatggctgc atccccccca cctctccctg accctgtata tagcccagcc aggccccagg 2100
cagggccaac ccttctctc ttgtaataa agccctggga tcaact 2145

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<210> 460

<211> 2149

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2149)

<223> 3' terminal sequence

<220>

<221> misc_feature

<222> (1)..(2149)

<223> Transcription factor AP -4 (activating enhancer binding protein 4) (TFAP4)

<400> 460

```

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```
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<210> 461

<211> 6478

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(6478)

<223> 3' terminal sequence

<220>

<221> misc_feature

<222> (1)..(6478)

<223> Cyclin D2 (CCND2)

<400> 461

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gctctccct ccccttcaa aaaacaaaa cagaaaaacc ctttccagg ccgggaaag 240
caggaggag aggggccgccc gggctggcca tggagctgct gtgccacgag gtggaccgg 300
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<210> 462

<211> 3490

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3490)

<223> 3' terminal sequence

<220>

<221> misc_feature

<222> (1)..(3490)

<223> Junction plakoglobin (JUP)

<400> 462

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<210> 463

<211> 1355

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature
<222> (1)..(1355)
<223> 3' terminal sequence

<220>
<221> misc_feature
<222> (1)..(1355)
<223> Growth arrest and DNA -damage-inducible, alpha
(GADD45A)

<400> 463
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ccctgaacgg tgatggcatc tgaatgaaa taa ctgaacc aaattgcact gaagtttttg 840
aaataccttt gtagttactc aagcagttac tcctacact gatgcaagga ttacagaaac 900
tgatgccaaagg gggctgagtg agttcaacta catgttctgg gggcccgag atagatgact 960
ttgcagatgg aaagaggtga aaatgaagaa ggaagctgtg ttgaaacaga aaaataagtc 1020
aaaaggaaca aaaattacaa agaaccatgc aggaaggaaa actatgtatt aatttagaat 1080
ggttgagtta cattaaaata aaccaaatat gttaaagttt aagtgtgcag ccatagtttg 1140
ggtatttttg gtttatatgc cctcaagtaa aagaaaagcc gaaagggtta atcataattg 1200
aaaaccatat tttattgtat tttgatgaga tatt aaattc tcaaagtttt attataaatt 1260
ctactaagtt attttatgac atgaaaagtt atttatgcta taaatttttt gaaacacaat 1320
acctacaata aactggtatg aataattgca tcatt 1355

<210> 464
<211> 732
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(732)
<223> 3' terminal sequence

<220>
<221> misc_feature
<222> (1)..(732)
<223> Non-metastatic cells 1, protein (NM23A) expressed
in (NME1)

<400> 464
tgctgcgaac cacgtgggtc cggggcgctg ttccgggtgct ggcggtgca gccggagttc 60
aaacctaaag agctggaagg aacctgagcc aactgtgagc gtaccttcac tgcgatcaaa 120
ccagatgggg tccagcgggg tcttgtggga gagattatca agcgttttga gcagaaagga 180
ttccgccttg ttggcttgaa attcatgcaa gcttccgaag atcttctcaa ggaacactac 240
gttgacctga aggaccgtcc attctttgcc ggcctggtga aatacatgca ctcagggccg 300

290/292

gtagttgcc a tggctctggga ggggctgaat gtggtgaaga cgggccgagt catgctcggg 360
gagaccaacc ctgcagactc caagcctggg accatccgtg gagacttctg catacaagtt 420
ggcaggaaca ttatacatgg cagtgattct gtggagagtg cagagaagga gatcggcttg 480
tggtttcacc ctgaggaact ggtagattac acgagctgtg ctcagaactg gatctatgaa 540
tgacaggagg gcagaccaca ttgcttttca catccatttc cctccttcc catgggcaga 600
ggaccaggct gtaggaaatc tagttattta caggaacttc atcataattt g gaggggaagc 660
tcttgagct gtgagttctc cctgtacagt gttaccatcc ccgaccatct gattaaaatg 720
cttctccca gc

<210> 465

<211> 942

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(942)

<223> 3' terminal sequence

<220>

<221> misc_feature

<222> (1)..(942)

<223> Ribosomal protein L13 (RPL13) (ex BBC1)

<400> 465

ctttccgctc ggctgttttc ctgcgcagga gccgcagggc cgtaggcagc catggcgccc 60
agccggaatg gcatggtctt gaagcccccac ttccacaagg actggcagcg gcgcgtggcc 120
acgtgggttca accagccggc ccgtaagatc cgcagacgta aggcccgga agccaaggcg 180
cgccgcatcg ccccgcgccc cgcgtcgggt cccatccggc ccatcgtgag ctgccccacg 240
gttcgggtacc acacgaaggt gcgcgcgggc cgcggcttca gcttgaggga gctcagggtg 300
gccggcattc acaagaaggt ggcccggacc atcggcattt ctgtggatcc gaggaggcgg 360
aacaagtcca cggagtccct gcagaccaac gtgcagcggc tgaaggagta ccgctccaaa 420
ctcactctct tccccaggaa gccctcggcc cccaagaagg gagacagttc tgctgaagaa 480
ctgaaaactg ccaccagct gaccggaccg gtcattgccg tccggaacgt ctataagaag 540
gagaaagctc gagtcatac tgagggaagag aagaatttca aagccttcgc tagtctccgt 600
atggcccgtg ccaacgccc gctcttcggc atacgggcaa aaagagccaa ggaagccgca 660
gaacaggatg ttgaaaagaa aaaataaagc cctcctgggg acttggaatc agtcgggcag 720
tcatgctggg tctccacgtg gtgtgtttcg tgggaacaac tgggcctggg atggggcttc 780
actgctgtga cttcctctg ccaggggatt tggggctttc ttgaaagaca gtccaagccc 840
tggaataatg tttactttct gtgttgaagc actgttggtt gtttggttag tgactgatgt 900
aaaacggtt tcttggtggg aggttacaga ggctgacttc ag 942

<210> 466

<211> 755

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(755)

<223> 3' terminal sequence

<220>
<221> misc_feature
<222> (1)..(755)
<223> vascular endothelial growth factor B (VEGFB)m

<400> 466
caccatgagc cctctgctcc gccgcctgct gctcgccgca ctcctgcagc tggcccccgc 60
ccaggcccoct gtctccagc ctgatgcccc tggccaccag aggaaagtgg tgtcatggat 120
agatgtgtat actcgcgcta cctgccagcc ccgggagggtg gtggtgccct tgactgtgga 180
gctcatgggc accgtggcca aacagctggt gccagctgc gtgactgtgc agcgtgtgg 240
tggctgctgc cctgacgatg gcctggagtg tgtgccact gggcagcacc aagtccggat 300
gcagatcctc atgatccggt acccgagcag t cagctgggg gagatgtccc tggaagaaca 360
cagccagtgt gaatgcagac ctaaaaaaaaa ggacagtgtc gtgaagccag acagggtgc 420
cactccccac caccgtcccc agccccgttc tgttccgggc tgggactctg cccccggagc 480
accctcccca cctgacatca cccatccac tccagcccca ggcccctctg cccacgtgc 540
accagcacc accagcgccc tgacccccgg acctgccgcc gccgctgccg acgccgcagc 600
ttctccgtt gccaaagggcg gggcttagag ctcaaccag acacctgcag gtgccggaag 660
ctgcgaaggt gacacatggc ttctcagact cagcagggtg acttgcctca gaggctatat 720
cccagtgggg gaacaaagag gagcctggta aa aaa 755

<210> 467
<211> 1039
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1039)
<223> 3' terminal sequence

<220>
<221> misc_feature
<222> (1)..(1039)
<223> Laminin receptor 1 (67kD, ribosomal protein SA)
(LAMR1)

<400> 467
tgctgtctt ttccgtgcta cctgcagagg ggtccatacg gcgttgttct ggattcccg 60
cgtaacttaa agggaaactt tcacaatgtc cggagccctt gatgtcctgc aaatgaagga 120
ggaggatgtc cttaa gttcc ttgcagcagg aaccactta gttggcacca atcttgactt 180
ccagatggaa cagtacatct ataaaaggaa aagtgatggc atctatatca taaatctcaa 240
gaggacctgg gagaagcttc tgctggcagc tcgtgcaatt gttgccattg aaaaccctgc 300
tgatgtcagt gttatatct ccaggaatac tggccagagg gctgtgctg a agtttgctgc 360
tgccactgga gccactccaa ttgctggccg cttcactcct ggaaccttca ctaaccagat 420
ccaggcagcc ttccgggagc cagggcttct tgtggttact gacccaggg ctgaccacca 480
gcctctcacg gaggcatctt atgttaacct acctaccatt gcgctgtgta acacagattc 540
tcctctgcgc tatgtg gaca ttgccatccc atgcaacaac aaggagctc actcagtggg 600
tttaatgtgg tggatgctgg ctcggaagt tctgcgcag cgtggcacca tttcccgta 660
acacccatgg gaggtcatgc ctgatctgta cttctacaga gatcctgaag agattgaaa 720
agaagagcag gctgtgctg agaaggcagt gaccaaggag gaatttcagg gtgaatggac 780
tgctcccgtc cctgagttca ctgctactca gcctgagggt gcagactggt ctgaagggtg 840
acaggtgccc tctgtgcta ttcagcaatt ccctactgaa gactggagcg ctcagcctgc 900
cacggaagac tggctgcag ctccactgc ttaggccact gaattggtag gagcaaccac 960
tgactgtct taagctg ttc ttgcataggc tcttaagcag catggaaaaa tggttgatgg 1020
aaaataaaca tcagtttct 1039

<210> 468
<211> 240
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(240)
<223> 3' terminal sequence

<220>
<221> misc_feature
<222> (1)..(240)
<223> Chorionic somatomammotropin hormone 1 (placental
lactogen) = LACTOGEN Precursor

<400> 468
attcggcagc atgactggcc aggggtataaa aaggggccac aagagac cgg ctctaggatc 60
ccaaggccca actccccgaa ccaactcaggg tcctgtggca gctcacctag tggcaatggc 120
tccaggetcc cggaaagctc ctgatactgg nttttgncct nctctnactg ccctggnttn 180
aanaagctng tgccttccaa ancgttcgt tatccagggt ttttgaccac gctatgctnc 240

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